

SEQUENCE LISTING

```

<110> Teijin Pharma Limited
      Komori, Toshihisa
      Kanatani, Naoko
      Yoshida, Carolina Andrea
      Zanma, Akira
      Kobayashi, Shinji
      Yamana, Kei

<120> BONE AND/OR JOINT-DISEASE-ASSOCIATES GENES

<130> Q94468

<150> PCT/JP2004/015879
<151> 2004-10-20

<150> JP 2003-359172
<151> 2003-10-20

<160> 114

<170> PatentIn version 3.1

<210> 1
<211> 5220
<212> DNA
<213> Mouse

<220>
<221> CDS
<222> (274)..(1962)

<400> 1
cggaactgct tcgactgcaa agcttcaagc gcagcctggg agcggcctgg tggccctatc      60
ccggcagctc cacacagcag aacgccctgg gtccctgaaa ctcgaaaccg gggctcagaa      120
ccagcggaaa ccaaagcgaa atccttgaac ttctctgaac aattgcttcc gggcgtttgc      180
tgagagccgg gggacctgac cggagcccgag gccgcgtatg gcgcgcccct gatgtcacac      240
ggacgccagc gaggccagcg ctccggctgc agc atg gac cgc gcg ggg cgc ctg      294
                               Met Asp Arg Ala Gly Arg Leu
                               1                               5

ggt gcg ggc ctg cgg gga ctc tgc gtg gct gca ctc gtg ctc gtg tgc      342
Gly Ala Gly Leu Arg Gly Leu Cys Val Ala Ala Leu Val Leu Val Cys
      10                               15                               20

gcc gga cac ggg ggc cgc cgc gag gat ggg gga cca gct tgc tac gga      390
Ala Gly His Gly Gly Arg Arg Glu Asp Gly Gly Pro Ala Cys Tyr Gly
      25                               30                               35

gga ttc gac ctc tac ttc atc ctg gac aag tca gga agt gtg ctg cac      438
Gly Phe Asp Leu Tyr Phe Ile Leu Asp Lys Ser Gly Ser Val Leu His
      40                               45                               50                               55

cac tgg aat gaa atc tac tac ttc gtg gag cag ttg gct cat aga ttc      486

```

His	Trp	Asn	Glu	Ile	Tyr	Tyr	Phe	Val	Glu	Gln	Leu	Ala	His	Arg	Phe	
				60					65					70		
atc	agc	cca	cag	cta	agg	atg	tcc	ttc	att	gtc	ttc	tct	act	cga	ggg	534
Ile	Ser	Pro	Gln	Leu	Arg	Met	Ser	Phe	Ile	Val	Phe	Ser	Thr	Arg	Gly	
			75					80					85			
aca	act	tta	atg	aaa	cta	act	gag	gac	agg	gaa	cag	atc	cga	caa	ggc	582
Thr	Thr	Leu	Met	Lys	Leu	Thr	Glu	Asp	Arg	Glu	Gln	Ile	Arg	Gln	Gly	
		90					95					100				
cta	gaa	gag	ctc	cag	aaa	gtt	ctg	cca	gga	gga	gac	act	tac	atg	cac	630
Leu	Glu	Glu	Leu	Gln	Lys	Val	Leu	Pro	Gly	Gly	Asp	Thr	Tyr	Met	His	
	105					110					115					
gaa	gga	ttc	gag	agg	gcc	agt	gag	cag	att	tac	tat	gag	aac	agt	caa	678
Glu	Gly	Phe	Glu	Arg	Ala	Ser	Glu	Gln	Ile	Tyr	Tyr	Glu	Asn	Ser	Gln	
120					125					130					135	
gga	tac	agg	acg	gcg	agc	gtc	atc	atc	gcg	ttg	acg	gat	ggg	gag	ctg	726
Gly	Tyr	Arg	Thr	Ala	Ser	Val	Ile	Ile	Ala	Leu	Thr	Asp	Gly	Glu	Leu	
				140					145					150		
cac	gag	gac	ctc	ttc	ttc	tac	tca	gag	agg	gag	gct	aac	cga	tcc	cga	774
His	Glu	Asp	Leu	Phe	Phe	Tyr	Ser	Glu	Arg	Glu	Ala	Asn	Arg	Ser	Arg	
			155					160					165			
gac	ctt	ggt	gcg	att	gtt	tac	tgc	gtt	ggc	gtg	aag	gat	ttc	aat	gaa	822
Asp	Leu	Gly	Ala	Ile	Val	Tyr	Cys	Val	Gly	Val	Lys	Asp	Phe	Asn	Glu	
		170					175					180				
act	cag	ttg	gct	cgg	att	gca	gac	agt	aag	gac	cac	gtg	ttt	cct	gtg	870
Thr	Gln	Leu	Ala	Arg	Ile	Ala	Asp	Ser	Lys	Asp	His	Val	Phe	Pro	Val	
	185					190					195					
aac	gac	ggc	ttc	cag	gct	ctc	caa	ggc	att	atc	cac	tca	att	tta	aag	918
Asn	Asp	Gly	Phe	Gln	Ala	Leu	Gln	Gly	Ile	Ile	His	Ser	Ile	Leu	Lys	
200					205					210					215	
aaa	tcc	tgc	atc	gaa	att	ctg	gcg	gct	gaa	cca	tcc	acc	atc	tgc	gcg	966
Lys	Ser	Cys	Ile	Glu	Ile	Leu	Ala	Ala	Glu	Pro	Ser	Thr	Ile	Cys	Ala	
				220					225					230		
gga	gag	tcc	ttt	caa	gtg	gtc	gta	aga	gga	aat	ggc	ttc	cga	cat	gcc	1014
Gly	Glu	Ser	Phe	Gln	Val	Val	Val	Arg	Gly	Asn	Gly	Phe	Arg	His	Ala	
			235					240					245			
cgc	aat	gtg	gac	agg	gtc	ctc	tgc	agc	ttc	aaa	atc	aat	gac	tca	gtc	1062
Arg	Asn	Val	Asp	Arg	Val	Leu	Cys	Ser	Phe	Lys	Ile	Asn	Asp	Ser	Val	
		250					255					260				
acg	ctc	aat	gag	aag	ccc	ttt	gct	gtg	gaa	gac	act	tat	ttg	ctg	tgc	1110
Thr	Leu	Asn	Glu	Lys	Pro	Phe	Ala	Val	Glu	Asp	Thr	Tyr	Leu	Leu	Cys	
	265					270					275					
cca	gca	cca	atc	ttg	aaa	gaa	gtt	ggc	atg	aaa	gct	gca	ctg	cag	gtc	1158
Pro	Ala	Pro	Ile	Leu	Lys	Glu	Val	Gly	Met	Lys	Ala	Ala	Leu	Gln	Val	
280					285					290					295	
agc	atg	aac	gac	ggc	ctg	tcc	ttc	atc	tcc	agt	tct	gtc	atc	atc	acc	1206

Ser	Met	Asn	Asp	Gly	Leu	Ser	Phe	Ile	Ser	Ser	Ser	Val	Ile	Ile	Thr	
				300					305					310		
acc	aca	cac	tgt	tca	gac	ggc	tcc	atc	ctg	gcg	att	gct	ctg	ctg	gtc	1254
Thr	Thr	His	Cys	Ser	Asp	Gly	Ser	Ile	Leu	Ala	Ile	Ala	Leu	Leu	Val	
			315					320					325			
ctc	ttc	ctg	ctg	ctg	gcc	ctg	gcg	ctg	ctc	tgg	tgg	ttc	tgg	ccc	ctc	1302
Leu	Phe	Leu	Leu	Leu	Ala	Leu	Ala	Leu	Leu	Trp	Trp	Phe	Trp	Pro	Leu	
		330					335					340				
tgc	tgc	aca	gtg	atc	atc	aag	gag	gtc	cct	cca	ccc	cct	ggt	gag	gag	1350
Cys	Cys	Thr	Val	Ile	Ile	Lys	Glu	Val	Pro	Pro	Pro	Pro	Val	Glu	Glu	
	345					350					355					
agt	gag	gaa	gaa	gac	gat	gat	ggg	ttg	cca	aag	aag	aaa	tgg	ccc	aca	1398
Ser	Glu	Glu	Glu	Asp	Asp	Asp	Gly	Leu	Pro	Lys	Lys	Lys	Trp	Pro	Thr	
360				365					370						375	
gta	gat	gcc	tct	tat	tat	ggg	gga	cg	ggg	gtg	gga	ggc	att	aaa	aga	1446
Val	Asp	Ala	Ser	Tyr	Tyr	Gly	Gly	Arg	Gly	Val	Gly	Gly	Ile	Lys	Arg	
				380					385					390		
atg	gag	gtc	cg	tgg	gga	gaa	aag	ggc	tcc	aca	gaa	gaa	ggg	gcg	aag	1494
Met	Glu	Val	Arg	Trp	Gly	Glu	Lys	Gly	Ser	Thr	Glu	Glu	Gly	Ala	Lys	
			395					400					405			
tta	gaa	aag	gca	aag	aat	gca	cga	gtc	aag	atg	cca	gag	caa	gaa	tat	1542
Leu	Glu	Lys	Ala	Lys	Asn	Ala	Arg	Val	Lys	Met	Pro	Glu	Gln	Glu	Tyr	
		410					415					420				
gag	ttc	cca	gaa	ccc	cga	aac	ctc	aac	aac	aac	atg	cg	cgg	cct	tcc	1590
Glu	Phe	Pro	Glu	Pro	Arg	Asn	Leu	Asn	Asn	Asn	Met	Arg	Arg	Pro	Ser	
	425					430					435					
tcg	cct	cg	aag	tgg	tac	tcg	ccc	atc	aag	gga	aaa	ctc	gat	gcc	ttg	1638
Ser	Pro	Arg	Lys	Trp	Tyr	Ser	Pro	Ile	Lys	Gly	Lys	Leu	Asp	Ala	Leu	
440					445				450						455	
tgg	gtt	ctg	ctg	aga	aaa	gga	tat	gac	cga	gtg	tct	gtg	atg	agg	cca	1686
Trp	Val	Leu	Leu	Arg	Lys	Gly	Tyr	Asp	Arg	Val	Ser	Val	Met	Arg	Pro	
				460				465						470		
cag	cca	gga	gac	acg	gga	cg	tgt	atc	aac	ttc	acc	aga	gtg	aag	aac	1734
Gln	Pro	Gly	Asp	Thr	Gly	Arg	Cys	Ile	Asn	Phe	Thr	Arg	Val	Lys	Asn	
			475					480					485			
agt	cag	cca	gcc	aag	tat	ccc	ctg	aac	aac	acc	tac	cac	ccc	agc	tcc	1782
Ser	Gln	Pro	Ala	Lys	Tyr	Pro	Leu	Asn	Asn	Thr	Tyr	His	Pro	Ser	Ser	
		490					495					500				
cca	cct	ccc	gct	cct	atc	tac	aca	ccc	cca	ccc	cct	gct	ccc	cac	tgc	1830
Pro	Pro	Pro	Ala	Pro	Ile	Tyr	Thr	Pro	Pro	Pro	Pro	Ala	Pro	His	Cys	
	505					510					515					
cct	ccc	cca	gcc	ccc	agt	gcc	ccc	act	cct	ccc	att	cct	tcc	cca	cca	1878
Pro	Pro	Pro	Ala	Pro	Ser	Ala	Pro	Thr	Pro	Pro	Ile	Pro	Ser	Pro	Pro	
520					525					530					535	
tcc	act	ctc	ccc	cct	cct	cct	cag	gcc	cca	ccc	cct	aac	agg	gca	cct	1926

Ser	Thr	Leu	Pro	Pro	Pro	Pro	Gln	Ala	Pro	Pro	Pro	Asn	Arg	Ala	Pro	
			540						545					550		
ccc	ccc	tcc	cga	cct	cct	cca	agg	cct	tct	gtc	tag	aacccaaagt				1972
Pro	Pro	Ser	Arg	Pro	Pro	Pro	Arg	Pro	Ser	Val						
			555						560							
ccgagctctg	ggctgcctga	gcaactccag	caggaggctt	ctctgctgaa	agaaagatct											2032
gcccagccta	tgtggtgagt	ggcggtgat	gtttgcacga	tttaaaagca	agtcgtgatg											2092
ggcagaacaa	aatgggcatt	ttgaactgcc	tgaagacaga	caatgagaca	ataacagtca											2152
cattatagcc	tgtgaccct	cacctctaga	ggaagggtcc	cgagatggcc	acattgccac											2212
agtgtctctca	gccagattat	gtcccatgaa	gaccaggaag	aaagtgactt	ccaagaatgg											2272
aatgcagcat	tggataagaa	acacctggct	gagattctga	cctcactgat	ttgactcttg											2332
attcttggac	tgggagccag	gccatctcca	cccttggtac	caccagcaa	ctctgaaaat											2392
gtgcagtgtc	cctagtatgc	atcgaatagg	tatccaactg	ggatctgcag	gttgccttat											2452
aaagagcata	tgctctattc	tctttccga	acttcttgt	ttcccagtga	tgagggaagg											2512
ggaaaggtgt	tgccatgctt	agaagttaga	ggacgtcagt	gctcagcact	gatggagaag											2572
cgttgatggg	agtgtccagc	tcttacatct	agaaatggct	ggcttcagca	ggcacagttc											2632
ctaaaccaac	aagccttgtc	attgtcaaag	gcaacctact	aatgattcac	cttaaacatc											2692
aagggttgact	gtggcatagg	tcagagctga	tcacacagaa	ccttccccat	gaaatcgcaa											2752
ggttcctcat	cttcaaatac	ccaggacccc	agagatttct	aaatccagct	aagagacagt											2812
agtcctgact	tggcaagaaa	accattccca	gttgttttac	tctgaaacag	gccgttgat											2872
gtatggtata	tctctccttg	gcctttcaac	ctgctcacia	gtattaccag	ttatgaagca											2932
aggagaaaata	catccagtgt	gtaatagaaa	agctctgccc	acaatcccca	tgtcactcct											2992
ctacattatt	ctgaagctgc	ttggctcagt	agccctttaa	cctcatgtag	actctggaca											3052
ctgtcaccca	atcatgaaaa	cagagggtcat	tgtcaaaggc	agtgtatagc	ctgtacaaaa											3112
atgatgcttc	cttcctcagt	ttccacaggc	cccaaaattc	ctgtcttagg	ctcctaaacc											3172
tctaaacttt	ttcctggaac	aaaagatata	aaacgggcat	aagtttttat	gttttgggct											3232
gtgatctcca	aagatccttc	aagaactcaa	gttagcctca	ttcttccagc	ttgttttagaa											3292
cagaggcatc	caggtgtcat	gcactccata	gacaccaatc	cttgttccca	aggcagacat											3352
tattaatcaa	tctcagcact	agttctcaat	ttaatccaat	tatatatttc	cacagtactt											3412
cacatctctt	atgacctgtt	ggtcactcagt	tagaattgag	agagataaac	actgtttgta											3472
atccctacct	tagaaagaaa	agcagaggag	aatgggggaa	ccaccagcat	aaaagttatt											3532
atctggggaa	aatcgacctg	aaagaacgcc	caagtccaag	acctatgggtg	ctgacaccaa											3592

agtaacactt	tcccaagtgt	accccagacc	ccactcttct	ccctgtggcc	accactccct	3652
gcttttcagg	agttgtgaaa	aagatctcct	tcacccttac	tgtgccccca	tattagaaca	3712
aggcttgttt	agtgtagtcc	ttgttaaaca	ggtgccagaa	tgtctcagcc	acctgagatg	3772
acattgctgg	gccccagaaa	accattccaa	ggagaatggg	ctccccaggc	tcagagcatg	3832
caactatgag	cccatggcaa	ctgttttgac	tgctggcagt	acaaaacggg	ccaccccaca	3892
ttacagctgc	aggatttggt	cagccataag	aaagtatgaa	ccaagatgct	ggtgttgctg	3952
ttcaacaagc	atgggcttcg	gggaaggcag	cagactccga	gagcaggcct	tgtgcagtgt	4012
cccaaggggc	tgtggtgaag	tgtctgagga	aaaatgaatg	ctgatacatg	gtgattctga	4072
gaagaatttg	caaggtttga	ccttagaatt	tatggaatgt	cttccctggg	cattcagaat	4132
tatggctaga	agtttctaga	aaccgtcaag	gttaatacct	ttcagagtag	gtgattacag	4192
gcaggaagag	ctttgatgtg	gtttacaaag	cccatcagtt	ctgtgtcatt	ccctgtaagc	4252
aacaggagat	ggtggttggt	attagcaaac	tgcattgtgt	atgtgtttga	ctccttggtt	4312
ttgtccttac	ggaggatttt	ttttatataa	gccaaatttt	gttgtatata	ttcatattcc	4372
acgtgacaga	tggaagcacg	tcctatcagt	gtgaataaaa	agaacagttg	tagtaaatta	4432
ttaaagccag	tgatttcatg	gcaggttacc	ctaccaagct	gtgcttggtg	atctcccatg	4492
accatactgc	ttttacaatg	tacaaatagt	tcctaggtga	cgagaccctc	ctttacataa	4552
tgccgatgac	agccttgctg	ggaactgcgg	tccttctgct	gtgacagcca	gctcgaaaac	4612
aggtcctgcc	tggagcttgc	cacacacttt	agggagacat	aagagctgtc	tttccccagc	4672
gtcagggaca	aagctaccat	aaagaagtgg	aaaagtcttg	gctctccagc	ctgggacaga	4732
ggtctctctg	gaaccccaag	gaagagcaga	aatgatcctt	gcctgccact	gcacacaatg	4792
tgatggtgga	aaatccatca	aggaataatt	gtgagataat	gaccgacagt	tcaggcgcaa	4852
agggaattca	tgctgtgtaa	agtgggtgga	attcgtttgc	aagctatgca	aagcctgatc	4912
ttactcacca	ggaggatgga	aagggttttt	ttagttatct	gagctcagct	gagttatcac	4972
gcttgagaaa	ccgatttaaa	ggaattagaa	tatgatttct	gaatacacat	aacattaaac	5032
tcttctcttt	ttctatggta	atthagttat	ggacgttcag	cgtctctgag	ttattggtat	5092
aaaagacttg	tcatcaccgc	actgtgctgt	aggagactgg	gctgaacctg	tacaatggta	5152
taccctggaa	gttgcttttt	taaaaaaaaa	taataataaa	cacctaaaat	caaaaaaaaa	5212
aaaaaaaa						5220

<210> 2
<211> 562

<212> PRT
<213> Mouse

<400> 2

Met Asp Arg Ala Gly Arg Leu Gly Ala Gly Leu Arg Gly Leu Cys Val
1 5 10 15

Ala Ala Leu Val Leu Val Cys Ala Gly His Gly Gly Arg Arg Glu Asp
20 25 30

Gly Gly Pro Ala Cys Tyr Gly Gly Phe Asp Leu Tyr Phe Ile Leu Asp
35 40 45

Lys Ser Gly Ser Val Leu His His Trp Asn Glu Ile Tyr Tyr Phe Val
50 55 60

Glu Gln Leu Ala His Arg Phe Ile Ser Pro Gln Leu Arg Met Ser Phe
65 70 75 80

Ile Val Phe Ser Thr Arg Gly Thr Thr Leu Met Lys Leu Thr Glu Asp
85 90 95

Arg Glu Gln Ile Arg Gln Gly Leu Glu Glu Leu Gln Lys Val Leu Pro
100 105 110

Gly Gly Asp Thr Tyr Met His Glu Gly Phe Glu Arg Ala Ser Glu Gln
115 120 125

Ile Tyr Tyr Glu Asn Ser Gln Gly Tyr Arg Thr Ala Ser Val Ile Ile
130 135 140

Ala Leu Thr Asp Gly Glu Leu His Glu Asp Leu Phe Phe Tyr Ser Glu
145 150 155 160

Arg Glu Ala Asn Arg Ser Arg Asp Leu Gly Ala Ile Val Tyr Cys Val
165 170 175

Gly Val Lys Asp Phe Asn Glu Thr Gln Leu Ala Arg Ile Ala Asp Ser
180 185 190

Lys Asp His Val Phe Pro Val Asn Asp Gly Phe Gln Ala Leu Gln Gly
195 200 205

Ile Ile His Ser Ile Leu Lys Lys Ser Cys Ile Glu Ile Leu Ala Ala
210 215 220

Glu Pro Ser Thr Ile Cys Ala Gly Glu Ser Phe Gln Val Val Val Arg
 225 230 235 240

Gly Asn Gly Phe Arg His Ala Arg Asn Val Asp Arg Val Leu Cys Ser
 245 250 255

Phe Lys Ile Asn Asp Ser Val Thr Leu Asn Glu Lys Pro Phe Ala Val
 260 265 270

Glu Asp Thr Tyr Leu Leu Cys Pro Ala Pro Ile Leu Lys Glu Val Gly
 275 280 285

Met Lys Ala Ala Leu Gln Val Ser Met Asn Asp Gly Leu Ser Phe Ile
 290 295 300

Ser Ser Ser Val Ile Ile Thr Thr Thr His Cys Ser Asp Gly Ser Ile
 305 310 315 320

Leu Ala Ile Ala Leu Leu Val Leu Phe Leu Leu Leu Ala Leu Ala Leu
 325 330 335

Leu Trp Trp Phe Trp Pro Leu Cys Cys Thr Val Ile Ile Lys Glu Val
 340 345 350

Pro Pro Pro Pro Val Glu Glu Ser Glu Glu Glu Asp Asp Asp Gly Leu
 355 360 365

Pro Lys Lys Lys Trp Pro Thr Val Asp Ala Ser Tyr Tyr Gly Gly Arg
 370 375 380

Gly Val Gly Gly Ile Lys Arg Met Glu Val Arg Trp Gly Glu Lys Gly
 385 390 395 400

Ser Thr Glu Glu Gly Ala Lys Leu Glu Lys Ala Lys Asn Ala Arg Val
 405 410 415

Lys Met Pro Glu Gln Glu Tyr Glu Phe Pro Glu Pro Arg Asn Leu Asn
 420 425 430

Asn Asn Met Arg Arg Pro Ser Ser Pro Arg Lys Trp Tyr Ser Pro Ile
 435 440 445

Lys Gly Lys Leu Asp Ala Leu Trp Val Leu Leu Arg Lys Gly Tyr Asp
 450 455 460

Arg Val Ser Val Met Arg Pro Gln Pro Gly Asp Thr Gly Arg Cys Ile
465 470 475 480

Asn Phe Thr Arg Val Lys Asn Ser Gln Pro Ala Lys Tyr Pro Leu Asn
485 490 495

Asn Thr Tyr His Pro Ser Ser Pro Pro Pro Ala Pro Ile Tyr Thr Pro
500 505 510

Pro Pro Pro Ala Pro His Cys Pro Pro Pro Ala Pro Ser Ala Pro Thr
515 520 525

Pro Pro Ile Pro Ser Pro Pro Ser Thr Leu Pro Pro Pro Pro Gln Ala
530 535 540

Pro Pro Pro Asn Arg Ala Pro Pro Pro Ser Arg Pro Pro Pro Arg Pro
545 550 555 560

Ser Val

<210> 3
<211> 1734
<212> DNA
<213> Mouse

<220>
<221> CDS
<222> (257)..(1012)

<400> 3
cccacgcgtc cgcgctcctg atctccagag gaccccgggc tgggacaggg gccttggcga 60
ggctgcagct gctgtggcag tagcttggga tggaggtctt tcttgctggg aactgaggag 120
ctgagagggt cctgtcaggc tcctgtccta aactcttggc acttgcggtg gcttgggctt 180
cacacactgt cagacacctt cttggtggcc tcctcggcct caggtttgaa gctgggtcca 240
caagggacac ggtgac atg agg ggc aac cca ctg atc cat ctt ctg gcc att 292
Met Arg Gly Asn Pro Leu Ile His Leu Leu Ala Ile
1 5 10
tcc ttc ctc tgc att ctc tca atg gtg tat tcc cag ctg tgc cca gca 340
Ser Phe Leu Cys Ile Leu Ser Met Val Tyr Ser Gln Leu Cys Pro Ala
15 20 25
ccc tgt gcc tgt cct tgg aca cca ccc cag tgc cca ccg ggg gta ccc 388
Pro Cys Ala Cys Pro Trp Thr Pro Pro Gln Cys Pro Pro Gly Val Pro
30 35 40

ctg gtg ctg gat ggc tgt ggc tgc tgt cga gtg tgt gca cgg agg ctg Leu Val Leu Asp Gly Cys Gly Cys Cys Arg Val Cys Ala Arg Arg Leu 45 50 55 60	436
ggg gag tcc tgc gac cac ctg cat gtc tgc gac ccc agc cag ggc ctg Gly Glu Ser Cys Asp His Leu His Val Cys Asp Pro Ser Gln Gly Leu 65 70 75	484
gtt tgt cag cct ggg gca ggc ccc agt ggc cgt ggt gct gtg tgc ctc Val Cys Gln Pro Gly Ala Gly Pro Ser Gly Arg Gly Ala Val Cys Leu 80 85 90	532
ttc gaa gag gat gac ggg agc tgt gag gtg aat ggc cgc agg tac ctg Phe Glu Glu Asp Asp Gly Ser Cys Glu Val Asn Gly Arg Arg Tyr Leu 95 100 105	580
gat ggg gag acc ttt aaa ccc aat tgc agg gtt ttg tgc cgc tgt gat Asp Gly Glu Thr Phe Lys Pro Asn Cys Arg Val Leu Cys Arg Cys Asp 110 115 120	628
gac ggt ggt ttc acc tgc ctg ccg ctg tgc agt gag gat gtg cgg ctg Asp Gly Gly Phe Thr Cys Leu Pro Leu Cys Ser Glu Asp Val Arg Leu 125 130 135 140	676
ccc agc tgg gac tgc cca cgc ccc agg aga ata cag gtg cca gga agg Pro Ser Trp Asp Cys Pro Arg Pro Arg Arg Ile Gln Val Pro Gly Arg 145 150 155	724
tgc tgc ccc gag tgg gtg tgt gac cag gca gtg atg cag ccg gca atc Cys Cys Pro Glu Trp Val Cys Asp Gln Ala Val Met Gln Pro Ala Ile 160 165 170	772
cag ccc tcc tca gcc caa gga cac caa ctt tct gcc ctt gtc act cct Gln Pro Ser Ser Ala Gln Gly His Gln Leu Ser Ala Leu Val Thr Pro 175 180 185	820
gca tct gcc gat ggc ccc tgt cca aac tgg agc aca gcc tgg ggc ccc Ala Ser Ala Asp Gly Pro Cys Pro Asn Trp Ser Thr Ala Trp Gly Pro 190 195 200	868
tgc tca acc acc tgt ggg ttg ggc ata gcc acc cga gta tcc aac cag Cys Ser Thr Thr Cys Gly Leu Gly Ile Ala Thr Arg Val Ser Asn Gln 205 210 215 220	916
aac cga ttc tgc caa ctg gag atc cag cgt cgc ctg tgt ctg tcc aga Asn Arg Phe Cys Gln Leu Glu Ile Gln Arg Arg Leu Cys Leu Ser Arg 225 230 235	964
ccc tgc ctg gca tcc agg agc cac ggc tca tgg aac agt gcc ttc tag Pro Cys Leu Ala Ser Arg Ser His Gly Ser Trp Asn Ser Ala Phe 240 245 250	1012
agccattgcg gggatgtgga tacagggcct gccattctca gcaaagtgtcc ctaggaccag	1072
gccctggact gatggtagat gccctctccc atgctcttggt ctgcagttaa ctgtcctggg	1132
tggattcagt gtccagagcc tctgagcgat ccctgctctg tctgaggtgg gggaagcagg	1192
tgaccagctc catttctctg gattctgacc caggcttctg gggttctcctg gctagttcct	1252

caaaacttcc ctgtatgaaa aggacaacca aaaggacctt taaagctaag ctgtactggg 1312
 caagcctggc caccatgctg gggatagtga cagtaatagg taccaggcag cagattgcct 1372
 gaaacatcca ggtcccttct tggacttcta tgtgcttgtc ccaaagatta tgggtgacct 1432
 tgtaagtgtg cctttcctga tctgagaaca ccctgcccgg ctgggaagaa ttttctggga 1492
 acatgaagag atggaatcac actattctta agagcgtttg ccaagtccag gaacttgacc 1552
 tttgtatttg taaaaataca catctcttaa atgctcacia agcaagaggc tccacacttc 1612
 tggcaggcca gggcctttct cttcagcatg agagagacaa ggaacagtag agtaccctcc 1672
 tctggaggac tggcccggtc tgggaataaac acccaaataca agtgtggaaa aaaaaaaaaa 1732
 aa 1734

<210> 4
 <211> 251
 <212> PRT
 <213> Mouse

<400> 4

Met Arg Gly Asn Pro Leu Ile His Leu Leu Ala Ile Ser Phe Leu Cys
 1 5 10 15

Ile Leu Ser Met Val Tyr Ser Gln Leu Cys Pro Ala Pro Cys Ala Cys
 20 25 30

Pro Trp Thr Pro Pro Gln Cys Pro Pro Gly Val Pro Leu Val Leu Asp
 35 40 45

Gly Cys Gly Cys Cys Arg Val Cys Ala Arg Arg Leu Gly Glu Ser Cys
 50 55 60

Asp His Leu His Val Cys Asp Pro Ser Gln Gly Leu Val Cys Gln Pro
 65 70 75 80

Gly Ala Gly Pro Ser Gly Arg Gly Ala Val Cys Leu Phe Glu Glu Asp
 85 90 95

Asp Gly Ser Cys Glu Val Asn Gly Arg Arg Tyr Leu Asp Gly Glu Thr
 100 105 110

Phe Lys Pro Asn Cys Arg Val Leu Cys Arg Cys Asp Asp Gly Gly Phe
 115 120 125

Thr Cys Leu Pro Leu Cys Ser Glu Asp Val Arg Leu Pro Ser Trp Asp
 130 135 140

Cys Pro Arg Pro Arg Arg Ile Gln Val Pro Gly Arg Cys Cys Pro Glu
145 150 155 160

Trp Val Cys Asp Gln Ala Val Met Gln Pro Ala Ile Gln Pro Ser Ser
165 170 175

Ala Gln Gly His Gln Leu Ser Ala Leu Val Thr Pro Ala Ser Ala Asp
180 185 190

Gly Pro Cys Pro Asn Trp Ser Thr Ala Trp Gly Pro Cys Ser Thr Thr
195 200 205

Cys Gly Leu Gly Ile Ala Thr Arg Val Ser Asn Gln Asn Arg Phe Cys
210 215 220

Gln Leu Glu Ile Gln Arg Arg Leu Cys Leu Ser Arg Pro Cys Leu Ala
225 230 235 240

Ser Arg Ser His Gly Ser Trp Asn Ser Ala Phe
245 250

<210> 5
<211> 3548
<212> DNA
<213> Mouse

<220>
<221> CDS
<222> (88)..(2190)

<400> 5
actggaccgc ccctcgaccc gggctgtgct ttggtgttct taagtcgtgc cgcgtgcgca 60

acggtagtga cgcgttttac ccggagc atg gcg gat acc ggc ttg cgc cgc gtg 114
Met Ala Asp Thr Gly Leu Arg Arg Val
1 5

gtt ccc agc gac ctt tat ccc ctt gtg ctc aga ttt ctg cgg gat agc 162
Val Pro Ser Asp Leu Tyr Pro Leu Val Leu Arg Phe Leu Arg Asp Ser
10 15 20 25

caa ctc tcg gag gtg gcc agt aaa ttt gca aaa gcg acc ggc gct aca 210
Gln Leu Ser Glu Val Ala Ser Lys Phe Ala Lys Ala Thr Gly Ala Thr
30 35 40

cag cag gac gcc aat gcc tcg tcc ctc ttg gac atc tat agc ttc tgg 258
Gln Gln Asp Ala Asn Ala Ser Ser Leu Leu Asp Ile Tyr Ser Phe Trp
45 50 55

ctc aag tcc acc aaa gcc cca aag gtg aag tta cag tca aat gga cca 306

Leu	Lys	Ser	Thr	Lys	Ala	Pro	Lys	Val	Lys	Leu	Gln	Ser	Asn	Gly	Pro	
		60					65					70				
gtg	acc	aag	aag	gct	aag	aaa	gag	act	tca	tcc	agt	gac	agc	agt	gag	354
Val	Thr	Lys	Lys	Ala	Lys	Lys	Glu	Thr	Ser	Ser	Ser	Asp	Ser	Ser	Glu	
		75				80					85					
gac	agc	agt	gag	gac	gag	gac	aaa	aaa	gcc	cag	gga	ctt	ccc	aca	cag	402
Asp	Ser	Ser	Glu	Asp	Glu	Asp	Lys	Lys	Ala	Gln	Gly	Leu	Pro	Thr	Gln	
90					95					100					105	
aag	gct	gcc	gca	cag	gtc	aag	cga	gcc	agt	gtg	cct	cag	cat	gct	gga	450
Lys	Ala	Ala	Ala	Gln	Val	Lys	Arg	Ala	Ser	Val	Pro	Gln	His	Ala	Gly	
				110					115					120		
aag	gca	gca	gcc	aaa	gct	tca	gag	agc	agc	agt	agt	gaa	gaa	tcc	agt	498
Lys	Ala	Ala	Ala	Lys	Ala	Ser	Glu	Ser	Ser	Ser	Ser	Glu	Glu	Ser	Ser	
				125				130					135			
gag	gaa	gag	gaa	gag	gac	aaa	aag	aaa	aag	cct	gtc	cag	aag	gca	gct	546
Glu	Glu	Glu	Glu	Glu	Asp	Lys	Lys	Lys	Lys	Pro	Val	Gln	Lys	Ala	Ala	
				140			145					150				
aag	ccc	caa	gcc	aag	gca	gtc	aga	cct	cct	gcg	aag	aag	gca	gag	agc	594
Lys	Pro	Gln	Ala	Lys	Ala	Val	Arg	Pro	Pro	Ala	Lys	Lys	Ala	Glu	Ser	
	155					160					165					
tct	gag	tcg	gac	tca	gac	tcg	gat	tcg	gac	tcc	agc	tca	gag	gaa	gaa	642
Ser	Glu	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Ser	Ser	Glu	Glu	Glu	
170					175					180					185	
aca	cca	cag	acc	cag	aag	cca	aag	gca	gct	gtg	gca	gca	aaa	gct	cag	690
Thr	Pro	Gln	Thr	Gln	Lys	Pro	Lys	Ala	Ala	Val	Ala	Ala	Lys	Ala	Gln	
				190					195					200		
act	aaa	gcc	gaa	gcc	aaa	cca	ggc	aca	cca	gcg	aaa	gca	cag	cct	aag	738
Thr	Lys	Ala	Glu	Ala	Lys	Pro	Gly	Thr	Pro	Ala	Lys	Ala	Gln	Pro	Lys	
			205					210					215			
gta	gcc	aat	ggc	aaa	gca	gcc	gcc	agc	agc	agc	agc	agc	agc	agc	agc	786
Val	Ala	Asn	Gly	Lys	Ala	Ala	Ala	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	
		220					225					230				
gat	gac	tca	gag	gaa	gag	aag	aag	gca	gct	gca	cct	ccc	aag	aag	act	834
Asp	Asp	Ser	Glu	Glu	Glu	Lys	Lys	Ala	Ala	Ala	Pro	Pro	Lys	Lys	Thr	
		235				240					245					
gta	cca	aaa	aag	caa	gtc	gtg	gcc	aag	gcc	cca	gtg	aaa	gta	gct	gcc	882
Val	Pro	Lys	Lys	Gln	Val	Val	Ala	Lys	Ala	Pro	Val	Lys	Val	Ala	Ala	
					255					260					265	
gcc	ccc	acc	cag	aag	agc	tcc	agc	agt	gag	gat	tct	tcc	agt	gaa	gag	930
Ala	Pro	Thr	Gln	Lys	Ser	Ser	Ser	Ser	Glu	Asp	Ser	Ser	Ser	Glu	Glu	
				270					275					280		
gag	gag	gga	cag	aga	caa	ccc	atg	aag	aaa	aaa	gca	ggc	ccc	tac	agt	978
Glu	Glu	Gly	Gln	Arg	Gln	Pro	Met	Lys	Lys	Lys	Ala	Gly	Pro	Tyr	Ser	
			285					290					295			
tca	gtt	cca	cca	ccc	tct	gtt	cct	tta	cca	aag	aag	tcc	ccg	gga	acc	1026

Ser	Val	Pro	Pro	Pro	Ser	Val	Pro	Leu	Pro	Lys	Lys	Ser	Pro	Gly	Thr		
		300					305					310					
cag	gct	cca	aag	aaa	gct	gct	gcg	cag	aca	cag	cct	gca	gac	agc	agt	1074	
Gln	Ala	Pro	Lys	Lys	Ala	Ala	Ala	Gln	Thr	Gln	Pro	Ala	Asp	Ser	Ser		
	315					320					325						
gac	gac	agc	agt	gac	gat	tct	gat	tca	agt	tct	gag	gaa	gag	aaa	aaa	1122	
Asp	Asp	Ser	Ser	Asp	Asp	Ser	Asp	Ser	Ser	Ser	Glu	Glu	Glu	Lys	Lys		
	330				335					340					345		
cct	cca	gct	aag	acg	gtc	gtc	tcc	aag	aca	ccc	gcc	aaa	gca	gct	cca	1170	
Pro	Pro	Ala	Lys	Thr	Val	Val	Ser	Lys	Thr	Pro	Ala	Lys	Ala	Ala	Pro		
				350					355					360			
gtg	aag	aag	aaa	gca	gaa	agc	tct	tca	gac	agc	tcg	gat	tct	gac	agt	1218	
Val	Lys	Lys	Lys	Ala	Glu	Ser	Ser	Ser	Asp	Ser	Ser	Asp	Ser	Asp	Ser		
			365					370					375				
tct	gag	gat	gaa	gct	cct	gcc	aag	cca	gtc	agt	aca	acc	aag	agt	ccc	1266	
Ser	Glu	Asp	Glu	Ala	Pro	Ala	Lys	Pro	Val	Ser	Thr	Thr	Lys	Ser	Pro		
		380					385						390				
aag	cca	gct	gtc	act	ccg	aag	cca	tct	gca	gca	aag	gca	gtg	aca	act	1314	
Lys	Pro	Ala	Val	Thr	Pro	Lys	Pro	Ser	Ala	Ala	Lys	Ala	Val	Thr	Thr		
		395				400					405						
cct	aag	caa	cct	gca	ggc	agt	aac	cag	aaa	cct	cag	agc	agg	aag	gct	1362	
Pro	Lys	Gln	Pro	Ala	Gly	Ser	Asn	Gln	Lys	Pro	Gln	Ser	Arg	Lys	Ala		
	410				415					420					425		
gac	agc	agc	tcc	agc	gag	gag	gaa	agc	agc	tcc	agc	gag	gag	gag	gag	1410	
Asp	Ser	Ser	Ser	Ser	Glu	Glu	Glu	Ser	Ser	Ser	Ser	Glu	Glu	Glu	Glu		
				430					435					440			
gcc	tcc	aag	aaa	agt	gcc	aca	acc	ccc	aag	gcc	aag	gtg	act	gct	aaa	1458	
Ala	Ser	Lys	Lys	Ser	Ala	Thr	Thr	Pro	Lys	Ala	Lys	Val	Thr	Ala	Lys		
			445					450					455				
gca	gca	ccc	gcc	aaa	cag	gcc	cct	cag	gct	gct	ggg	gac	agc	agc	tct	1506	
Ala	Ala	Pro	Ala	Lys	Gln	Ala	Pro	Gln	Ala	Ala	Gly	Asp	Ser	Ser	Ser		
		460					465					470					
gac	tca	gat	agt	tcc	agc	agt	gaa	gag	gag	gag	aag	act	cct	aag	ccc	1554	
Asp	Ser	Asp	Ser	Ser	Ser	Ser	Glu	Glu	Glu	Glu	Lys	Thr	Pro	Lys	Pro		
		475				480					485						
cca	gct	aag	aag	aag	gca	gca	ggt	gga	gcc	gtt	tct	aca	cca	gcc	cct	1602	
Pro	Ala	Lys	Lys	Lys	Ala	Ala	Gly	Gly	Ala	Val	Ser	Thr	Pro	Ala	Pro		
					495					500					505		
ggg	aag	aaa	gca	gag	gcc	aag	agc	agc	agc	agc	agc	agc	agc	agc	agc	1650	
Gly	Lys	Lys	Ala	Glu	Ala	Lys	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser		
				510					515					520			
tcc	gaa	gat	tcc	agt	gaa	gag	gag	aaa	aaa	aag	aag	ccc	aaa	gct	act	1698	
Ser	Glu	Asp	Ser	Ser	Glu	Glu	Glu	Lys	Lys	Lys	Lys	Pro	Lys	Ala	Thr		
			525					530					535				
acc	cct	aaa	ata	cag	gca	agc	aag	gcc	aat	ggc	act	cca	gct	tct	ctg	1746	

Thr	Pro	Lys	Ile	Gln	Ala	Ser	Lys	Ala	Asn	Gly	Thr	Pro	Ala	Ser	Leu	
		540					545					550				
aat	gga	aaa	gca	gcc	aag	gaa	agt	gag	gag	gaa	gag	gag	gag	gaa	gaa	1794
Asn	Gly	Lys	Ala	Ala	Lys	Glu	Ser	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	
		555				560					565					
aca	gaa	gag	aag	aaa	aag	gca	gct	ggg	acc	aag	cca	ggt	tca	ggc	aaa	1842
Thr	Glu	Glu	Lys	Lys	Lys	Ala	Ala	Gly	Thr	Lys	Pro	Gly	Ser	Gly	Lys	
570					575					580					585	
aaa	cgg	aag	cag	aat	gag	acc	gca	gat	gaa	gca	aca	act	cct	caa	gct	1890
Lys	Arg	Lys	Gln	Asn	Glu	Thr	Ala	Asp	Glu	Ala	Thr	Thr	Pro	Gln	Ala	
			590						595					600		
aag	aaa	gtt	aag	ctc	gag	acc	ccc	aat	acg	ttt	cca	aaa	agg	aag	aag	1938
Lys	Lys	Val	Lys	Leu	Glu	Thr	Pro	Asn	Thr	Phe	Pro	Lys	Arg	Lys	Lys	
		605						610					615			
gga	gaa	aga	agg	gcg	tct	tcc	cct	ttc	cga	agg	gtc	agg	gag	gag	gag	1986
Gly	Glu	Arg	Arg	Ala	Ser	Ser	Pro	Phe	Arg	Arg	Val	Arg	Glu	Glu	Glu	
		620					625					630				
att	gag	gtg	gac	tct	cga	gtg	gcg	gac	aat	tcc	ttt	gat	gcc	aag	cga	2034
Ile	Glu	Val	Asp	Ser	Arg	Val	Ala	Asp	Asn	Ser	Phe	Asp	Ala	Lys	Arg	
		635				640					645					
ggt	gca	gct	gga	gac	tgg	ggg	gag	cga	gcc	aat	cag	gtt	ctg	aag	ttc	2082
Gly	Ala	Ala	Gly	Asp	Trp	Gly	Glu	Arg	Ala	Asn	Gln	Val	Leu	Lys	Phe	
650					655					660					665	
acc	aaa	ggc	aag	tcc	ttc	cgg	cat	gaa	aaa	acg	aag	aag	aag	cga	ggc	2130
Thr	Lys	Gly	Lys	Ser	Phe	Arg	His	Glu	Lys	Thr	Lys	Lys	Lys	Arg	Gly	
				670						675				680		
agc	tac	cgg	gga	ggc	tcc	atc	tct	gtc	cag	gtc	aat	tcc	gtc	aaa	ttc	2178
Ser	Tyr	Arg	Gly	Gly	Ser	Ile	Ser	Val	Gln	Val	Asn	Ser	Val	Lys	Phe	
			685					690					695			
gac	agc	gag	tga	cacgtggtca	tccttttgga	aaggaagggt	gatttttgga									2230
Asp	Ser	Glu														
		700														
gactggcact	caactccagt	ggacccagaa	actccgtgtt	aggagacagt	tgtgacaagg											2290
acggtgtgga	gcaggtcctg	aggtgtgtca	gcctgcagtc	ctctcaggct	cctttttctg											2350
gacagctgaa	tatcaaggac	aaaaaggatt	ttttttttta	aagaaacca	ttcagttgtc											2410
aattgccttc	ctgttctgtg	ggtcttcata	ctgagagatt	tgtatatttt	atattaaatc											2470
atgtcataca	gatttttgtt	gtgattttca	gagatgactt	ccacagatta	aagtcttagc											2530
tgttgccctaa	ggcaaagcaa	aacaacacat	ggtaataatt	ttccctactg	gaggattctc											2590
tttatgtgaa	agccctggtg	ggcaatgaca	taagtcttgt	gatgattgtc	tgctaagcat											2650
actctgtgct	catcttcac	cattggggccc	ggcaccaaag	cttctagaag	ccagcgtgga											2710
tctaccaact	ttgggggata	aaattgccat	tcttggtgca	gtaacctact	aattggcagg											2770

caggattctc gagtgtgtga atgccatgca gctgtctttg ttttgttctt ggtagctggt 2830
actgctacat gtttacagta cttttagttt taatttcgaa gtaagctttt ctgacagaca 2890
ttttgcaaca acttgactgt tgtatattga caagttcatg gatgtatttg attcttatta 2950
acatcaagga caggctggta agtacctgca tgggtgagtc actggtcaag gaaatggaga 3010
tgacctatga accctgggtg gaagtagata cactggatct cctgggcacc tggagcagca 3070
gcaggagaca gccaaggag gcaggagggc tctaactaag caggaccatt ttgtcttgaa 3130
gtcgggtacac aggagtaatt atgccctggt caagttgggc ccctggactc actattagta 3190
ccttacctat aatgttactg atacagacta gccaggagggc agggaggcat agctgggtgg 3250
tagtgtgctt gcttagcatt catagaccaa gtgtgatctc tatcaccgca ggaagtaaag 3310
agcagagaga ttcctggggc aaggagtggt attataaagc tgtaggatgt gaccattggc 3370
agtgagggca ggggtgggac gtggctggcc tgggtgagaaa cggataccgg gcattgcctc 3430
ccctgtttgg tgtccacgct cacctggtaa cctgctaaaa gctgtggcag ctcttctgtg 3490
aaggctgcat ggtcaaagtt ctgtgtctta ccacaaaaca ataaagtga tggttcct 3548

<210> 6
<211> 700
<212> PRT
<213> Mouse

<400> 6

Met Ala Asp Thr Gly Leu Arg Arg Val Val Pro Ser Asp Leu Tyr Pro
1 5 10 15

Leu Val Leu Arg Phe Leu Arg Asp Ser Gln Leu Ser Glu Val Ala Ser
20 25 30

Lys Phe Ala Lys Ala Thr Gly Ala Thr Gln Gln Asp Ala Asn Ala Ser
35 40 45

Ser Leu Leu Asp Ile Tyr Ser Phe Trp Leu Lys Ser Thr Lys Ala Pro
50 55 60

Lys Val Lys Leu Gln Ser Asn Gly Pro Val Thr Lys Lys Ala Lys Lys
65 70 75 80

Glu Thr Ser Ser Ser Asp Ser Ser Glu Asp Ser Ser Glu Asp Glu Asp
85 90 95

Lys Lys Ala Gln Gly Leu Pro Thr Gln Lys Ala Ala Ala Gln Val Lys

100					105					110					
Arg	Ala	Ser	Val	Pro	Gln	His	Ala	Gly	Lys	Ala	Ala	Ala	Lys	Ala	Ser
		115					120						125		
Glu	Ser	Ser	Ser	Ser	Glu	Glu	Ser	Ser	Glu	Glu	Glu	Glu	Glu	Asp	Lys
	130					135					140				
Lys	Lys	Lys	Pro	Val	Gln	Lys	Ala	Ala	Lys	Pro	Gln	Ala	Lys	Ala	Val
145					150					155					160
Arg	Pro	Pro	Ala	Lys	Lys	Ala	Glu	Ser	Ser	Glu	Ser	Asp	Ser	Asp	Ser
				165					170					175	
Asp	Ser	Asp	Ser	Ser	Ser	Glu	Glu	Glu	Thr	Pro	Gln	Thr	Gln	Lys	Pro
			180					185					190		
Lys	Ala	Ala	Val	Ala	Ala	Lys	Ala	Gln	Thr	Lys	Ala	Glu	Ala	Lys	Pro
	195						200					205			
Gly	Thr	Pro	Ala	Lys	Ala	Gln	Pro	Lys	Val	Ala	Asn	Gly	Lys	Ala	Ala
	210					215					220				
Ala	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Asp	Asp	Ser	Glu	Glu	Glu	Lys
225					230					235					240
Lys	Ala	Ala	Ala	Pro	Pro	Lys	Lys	Thr	Val	Pro	Lys	Lys	Gln	Val	Val
				245					250					255	
Ala	Lys	Ala	Pro	Val	Lys	Val	Ala	Ala	Ala	Pro	Thr	Gln	Lys	Ser	Ser
			260					265					270		
Ser	Ser	Glu	Asp	Ser	Ser	Ser	Glu	Glu	Glu	Glu	Gly	Gln	Arg	Gln	Pro
		275					280					285			
Met	Lys	Lys	Lys	Ala	Gly	Pro	Tyr	Ser	Ser	Val	Pro	Pro	Pro	Ser	Val
	290					295					300				
Pro	Leu	Pro	Lys	Lys	Ser	Pro	Gly	Thr	Gln	Ala	Pro	Lys	Lys	Ala	Ala
305					310					315					320
Ala	Gln	Thr	Gln	Pro	Ala	Asp	Ser	Ser	Asp	Asp	Ser	Ser	Asp	Asp	Ser
				325					330					335	
Asp	Ser	Ser	Ser	Glu	Glu	Glu	Lys	Lys	Pro	Pro	Ala	Lys	Thr	Val	Val

340					345					350					
Ser	Lys	Thr	Pro	Ala	Lys	Ala	Ala	Pro	Val	Lys	Lys	Lys	Ala	Glu	Ser
		355					360					365			
Ser	Ser	Asp	Ser	Ser	Asp	Ser	Asp	Ser	Ser	Glu	Asp	Glu	Ala	Pro	Ala
	370					375					380				
Lys	Pro	Val	Ser	Thr	Thr	Lys	Ser	Pro	Lys	Pro	Ala	Val	Thr	Pro	Lys
385						390					395				400
Pro	Ser	Ala	Ala	Lys	Ala	Val	Thr	Thr	Pro	Lys	Gln	Pro	Ala	Gly	Ser
				405					410					415	
Asn	Gln	Lys	Pro	Gln	Ser	Arg	Lys	Ala	Asp	Ser	Ser	Ser	Ser	Glu	Glu
			420					425						430	
Glu	Ser	Ser	Ser	Ser	Glu	Glu	Glu	Glu	Ala	Ser	Lys	Lys	Ser	Ala	Thr
		435					440						445		
Thr	Pro	Lys	Ala	Lys	Val	Thr	Ala	Lys	Ala	Ala	Pro	Ala	Lys	Gln	Ala
	450					455					460				
Pro	Gln	Ala	Ala	Gly	Asp	Ser	Ser	Ser	Asp	Ser	Asp	Ser	Ser	Ser	Ser
465						470					475				480
Glu	Glu	Glu	Glu	Lys	Thr	Pro	Lys	Pro	Pro	Ala	Lys	Lys	Lys	Ala	Ala
				485					490					495	
Gly	Gly	Ala	Val	Ser	Thr	Pro	Ala	Pro	Gly	Lys	Lys	Ala	Glu	Ala	Lys
			500					505					510		
Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Glu	Asp	Ser	Ser	Glu	Glu
		515					520					525			
Glu	Lys	Lys	Lys	Lys	Pro	Lys	Ala	Thr	Thr	Pro	Lys	Ile	Gln	Ala	Ser
	530					535					540				
Lys	Ala	Asn	Gly	Thr	Pro	Ala	Ser	Leu	Asn	Gly	Lys	Ala	Ala	Lys	Glu
545						550					555				560
Ser	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Thr	Glu	Glu	Lys	Lys	Lys	Ala
				565					570					575	
Ala	Gly	Thr	Lys	Pro	Gly	Ser	Gly	Lys	Lys	Arg	Lys	Gln	Asn	Glu	Thr

580					585					590						
Ala	Asp	Glu	Ala	Thr	Thr	Pro	Gln	Ala	Lys	Lys	Val	Lys	Leu	Glu	Thr	
595					600					605						
Pro	Asn	Thr	Phe	Pro	Lys	Arg	Lys	Lys	Gly	Glu	Arg	Arg	Ala	Ser	Ser	
610					615					620						
Pro	Phe	Arg	Arg	Val	Arg	Glu	Glu	Glu	Ile	Glu	Val	Asp	Ser	Arg	Val	
625					630					635					640	
Ala	Asp	Asn	Ser	Phe	Asp	Ala	Lys	Arg	Gly	Ala	Ala	Gly	Asp	Trp	Gly	
645					650					655						
Glu	Arg	Ala	Asn	Gln	Val	Leu	Lys	Phe	Thr	Lys	Gly	Lys	Ser	Phe	Arg	
660					665					670						
His	Glu	Lys	Thr	Lys	Lys	Lys	Arg	Gly	Ser	Tyr	Arg	Gly	Gly	Ser	Ile	
675					680					685						
Ser	Val	Gln	Val	Asn	Ser	Val	Lys	Phe	Asp	Ser	Glu					
690					695					700						

<210> 7
 <211> 4126
 <212> DNA
 <213> Mouse

<220>
 <221> CDS
 <222> (16)..(4050)

<400> 7	
cgtgtttggc tcagc atg gcg gag atg aag agc cct acg aaa gct gag cct	51
Met Ala Glu Met Lys Ser Pro Thr Lys Ala Glu Pro	
1 5 10	
gcg act ccc gca gaa gcg gcg caa agc gac cgc cac agc ctg ctg gag	99
Ala Thr Pro Ala Glu Ala Ala Gln Ser Asp Arg His Ser Leu Leu Glu	
15 20 25	
cac agc cgc gag ttc ttg gac ttc ttc tgg gac att gcg aaa ccg gat	147
His Ser Arg Glu Phe Leu Asp Phe Phe Trp Asp Ile Ala Lys Pro Asp	
30 35 40	
cag gaa acg cgg ctc cgg gcc acg gag aag ttg ttg gag tac ttg cgc	195
Gln Glu Thr Arg Leu Arg Ala Thr Glu Lys Leu Leu Glu Tyr Leu Arg	
45 50 55 60	
aca agg ccc aat gat tcg gag atg aaa tat gcc ctg aag cgc cta atc	243
Thr Arg Pro Asn Asp Ser Glu Met Lys Tyr Ala Leu Lys Arg Leu Ile	

65										70					75					
act	ggg	ctt	ggg	gtg	ggc	cga	gaa	gcc	gct	acg	gcc	tgc	tac	agc	ctg	291				
Thr	Gly	Leu	Gly	Val	Gly	Arg	Glu	Ala	Ala	Thr	Ala	Cys	Tyr	Ser	Leu					
		80						85				90								
gcg	ctg	gca	cag	ctg	ttg	cag	tct	ttt	gaa	gac	atc	cca	ttg	tgt	gac	339				
Ala	Leu	Ala	Gln	Leu	Leu	Gln	Ser	Phe	Glu	Asp	Ile	Pro	Leu	Cys	Asp					
		95					100					105								
atc	ctg	gat	cag	ata	caa	gaa	aaa	tac	agc	cta	caa	gcc	atg	aac	aag	387				
Ile	Leu	Asp	Gln	Ile	Gln	Glu	Lys	Tyr	Ser	Leu	Gln	Ala	Met	Asn	Lys					
	110					115					120									
gca	atg	atg	aga	cct	agt	ctc	ttt	gca	aac	ctt	ttt	gga	gtg	cta	gcc	435				
Ala	Met	Met	Arg	Pro	Ser	Leu	Phe	Ala	Asn	Leu	Phe	Gly	Val	Leu	Ala					
	125				130					135					140					
ctc	ttt	cag	tca	ggc	cgc	cta	gtg	aag	gac	aaa	gag	gcc	ctg	atg	aag	483				
Leu	Phe	Gln	Ser	Gly	Arg	Leu	Val	Lys	Asp	Lys	Glu	Ala	Leu	Met	Lys					
				145					150					155						
tcc	gtg	caa	ttg	ctg	aag	atc	ctg	tcc	caa	cac	ccc	aac	cac	tta	cag	531				
Ser	Val	Gln	Leu	Leu	Lys	Ile	Leu	Ser	Gln	His	Pro	Asn	His	Leu	Gln					
			160					165						170						
gga	cag	cca	ata	aag	gct	ctg	gtg	gac	atc	ctc	tct	gag	gtc	cca	gag	579				
Gly	Gln	Pro	Ile	Lys	Ala	Leu	Val	Asp	Ile	Leu	Ser	Glu	Val	Pro	Glu					
		175					180					185								
tcc	atg	ttc	cag	gag	atc	ctg	cca	aag	gtc	ctc	aag	ggt	aac	atg	aaa	627				
Ser	Met	Phe	Gln	Glu	Ile	Leu	Pro	Lys	Val	Leu	Lys	Gly	Asn	Met	Lys					
	190					195					200									
gtg	atc	ctc	cgc	tct	ccc	aag	tac	ttg	gag	ctc	ttc	ctc	ctg	gct	aag	675				
Val	Ile	Leu	Arg	Ser	Pro	Lys	Tyr	Leu	Glu	Leu	Phe	Leu	Leu	Ala	Lys					
	205				210					215					220					
cag	agg	gtg	ccg	aca	aag	ctc	gag	tca	ctc	atg	ggc	tcg	gtt	gac	cta	723				
Gln	Arg	Val	Pro	Thr	Lys	Leu	Glu	Ser	Leu	Met	Gly	Ser	Val	Asp	Leu					
				225					230					235						
ttc	tca	gaa	gac	aat	att	ccc	agt	ctg	gtg	aac	atc	ctg	aag	gtg	gcc	771				
Phe	Ser	Glu	Asp	Asn	Ile	Pro	Ser	Leu	Val	Asn	Ile	Leu	Lys	Val	Ala					
			240					245					250							
gcc	aac	tct	gtc	aag	aag	gag	cac	aag	ctg	cct	aat	gtg	gct	ctg	gac	819				
Ala	Asn	Ser	Val	Lys	Lys	Glu	His	Lys	Leu	Pro	Asn	Val	Ala	Leu	Asp					
		255					260					265								
ctg	ctc	cgc	ctg	gct	ctc	aag	gag	agc	aga	ttc	gaa	ctg	ttc	tgg	aag	867				
Leu	Leu	Arg	Leu	Ala	Leu	Lys	Glu	Ser	Arg	Phe	Glu	Leu	Phe	Trp	Lys					
		270				275					280									
aag	gtt	ttg	gag	gag	ggg	ctg	ctg	aag	aat	ccg	tcc	tgg	aca	tcc	agc	915				
Lys	Val	Leu	Glu	Glu	Gly	Leu	Leu	Lys	Asn	Pro	Ser	Trp	Thr	Ser	Ser					
	285				290					295					300					
tac	atg	tgc	ttc	cgc	cta	ctg	ggt	gcg	tct	ctg	ccg	ctt	ctg	tca	gag	963				
Tyr	Met	Cys	Phe	Arg	Leu	Leu	Gly	Ala	Ser	Leu	Pro	Leu	Leu	Ser	Glu					

305										310					315					
gag	cag	ttg	cag	ttg	gtg	atg	cga	gga	gac	ttg	atc	cgc	cat	ttt	ggg	1011				
Glu	Gln	Leu	Gln	Leu	Val	Met	Arg	Gly	Asp	Leu	Ile	Arg	His	Phe	Gly					
			320			325						330								
gag	aac	atg	gtt	att	tct	aag	ccc	caa	aac	cta	ttt	aag	atc	atc	cca	1059				
Glu	Asn	Met	Val	Ile	Ser	Lys	Pro	Gln	Asn	Leu	Phe	Lys	Ile	Ile	Pro					
			335			340						345								
gag	ata	agt	aca	tac	gtg	ggt	acc	ttc	cta	gag	ggg	tgc	cag	gat	gac	1107				
Glu	Ile	Ser	Thr	Tyr	Val	Gly	Thr	Phe	Leu	Glu	Gly	Cys	Gln	Asp	Asp					
			350			355						360								
cct	aag	cgg	cag	ttg	act	atg	atg	gtg	gcc	ttt	aca	acc	atc	acc	aat	1155				
Pro	Lys	Arg	Gln	Leu	Thr	Met	Met	Val	Ala	Phe	Thr	Thr	Ile	Thr	Asn					
			365			370						375			380					
caa	ggt	ctc	cct	gtc	atg	cct	acc	ttc	tgg	cgt	gtc	acg	cgg	ttt	ttg	1203				
Gln	Gly	Leu	Pro	Val	Met	Pro	Thr	Phe	Trp	Arg	Val	Thr	Arg	Phe	Leu					
			385						390						395					
aat	gct	gaa	gcc	ctg	cag	agc	tat	gtg	gcc	tgg	ttg	cgg	gac	atg	ttc	1251				
Asn	Ala	Glu	Ala	Leu	Gln	Ser	Tyr	Val	Ala	Trp	Leu	Arg	Asp	Met	Phe					
			400						405						410					
ctg	cag	cct	gac	ctg	aac	tcc	ttg	gtt	gac	ttc	agc	act	gcc	aac	cag	1299				
Leu	Gln	Pro	Asp	Leu	Asn	Ser	Leu	Val	Asp	Phe	Ser	Thr	Ala	Asn	Gln					
			415						420						425					
aag	aga	gct	cag	gac	gcc	tcg	ttg	aat	gtg	cct	gag	cga	gct	gta	ttc	1347				
Lys	Arg	Ala	Gln	Asp	Ala	Ser	Leu	Asn	Val	Pro	Glu	Arg	Ala	Val	Phe					
			430						435						440					
cgg	ctc	cgg	aag	tgg	atc	atc	cac	cgc	ctg	gtc	agc	ctt	gtg	gat	cat	1395				
Arg	Leu	Arg	Lys	Trp	Ile	Ile	His	Arg	Leu	Val	Ser	Leu	Val	Asp	His					
			445			450						455			460					
ttg	cat	ctg	gag	aag	gat	gaa	gct	gtg	gtt	gag	caa	ata	gcc	agg	ttt	1443				
Leu	His	Leu	Glu	Lys	Asp	Glu	Ala	Val	Val	Glu	Gln	Ile	Ala	Arg	Phe					
			465						470						475					
tgc	ttg	ttc	cat	gcc	ttc	ttt	aag	acg	aag	aag	gct	acg	ccc	cag	atc	1491				
Cys	Leu	Phe	His	Ala	Phe	Phe	Lys	Thr	Lys	Lys	Ala	Thr	Pro	Gln	Ile					
			480						485						490					
cca	gag	acg	aag	cag	cac	ttc	tcc	ttc	cct	ttg	gac	gac	cgc	aac	cgt	1539				
Pro	Glu	Thr	Lys	Gln	His	Phe	Ser	Phe	Pro	Leu	Asp	Asp	Arg	Asn	Arg					
			495			500						505								
ggg	gtc	ttt	gtc	agt	gcc	ttc	ttc	agc	cta	ctg	cag	acg	ctc	agt	gtg	1587				
Gly	Val	Phe	Val	Ser	Ala	Phe	Phe	Ser	Leu	Leu	Gln	Thr	Leu	Ser	Val					
			510			515						520								
aag	ttc	agg	cag	aca	cca	gac	ctg	gct	gaa	aat	ggg	aag	cct	tgg	act	1635				
Lys	Phe	Arg	Gln	Thr	Pro	Asp	Leu	Ala	Glu	Asn	Gly	Lys	Pro	Trp	Thr					
			525			530						535			540					
tac	cgc	ctg	gtt	cag	ttg	gca	gac	atg	ctg	ttg	aac	cat	aac	cgc	aat	1683				
Tyr	Arg	Leu	Val	Gln	Leu	Ala	Asp	Met	Leu	Leu	Asn	His	Asn	Arg	Asn					

545										550					555					
gta	acc	agt	gtg	aca	tcc	ttg	aca	aca	cag	cag	cgt	cag	gcc	tgg	gac	1731				
Val	Thr	Ser	Val	Thr	Ser	Leu	Thr	Thr	Gln	Gln	Arg	Gln	Ala	Trp	Asp					
			560						565			570								
cag	atg	atg	agt	act	ctg	aag	gaa	tta	gag	gcc	cgc	tcc	tct	gag	acc	1779				
Gln	Met	Met	Ser	Thr	Leu	Lys	Glu	Leu	Glu	Ala	Arg	Ser	Ser	Glu	Thr					
			575						580			585								
agg	gcc	att	gcc	ttc	cag	cac	ctg	ctg	ctt	ctg	gtg	ggc	ctc	cac	atc	1827				
Arg	Ala	Ile	Ala	Phe	Gln	His	Leu	Leu	Leu	Leu	Val	Gly	Leu	His	Ile					
			590						595			600								
ttc	aag	tcc	cct	gca	gaa	agc	tgt	gat	gtc	cta	gga	gac	att	cag	act	1875				
Phe	Lys	Ser	Pro	Ala	Glu	Ser	Cys	Asp	Val	Leu	Gly	Asp	Ile	Gln	Thr					
			605						610			615			620					
tgc	atc	aag	aaa	agc	atg	gag	cag	aat	ccc	cgc	cga	tca	cgc	tct	aga	1923				
Cys	Ile	Lys	Lys	Ser	Met	Glu	Gln	Asn	Pro	Arg	Arg	Ser	Arg	Ser	Arg					
			625						630			635								
gcc	aaa	gcc	tcc	cag	gag	cca	gta	tgg	gtg	gag	gtg	atg	gtg	gag	atc	1971				
Ala	Lys	Ala	Ser	Gln	Glu	Pro	Val	Trp	Val	Glu	Val	Met	Val	Glu	Ile					
			640						645			650								
ttg	ctg	tcc	ttg	ctg	gct	caa	ccc	agc	aac	ttg	atg	cgc	cag	gtg	gtc	2019				
Leu	Leu	Ser	Leu	Leu	Ala	Gln	Pro	Ser	Asn	Leu	Met	Arg	Gln	Val	Val					
			655						660			665								
cgg	agt	gta	ttt	ggc	cat	atc	tgt	ccc	cac	ctt	act	cca	cgt	tgt	ctg	2067				
Arg	Ser	Val	Phe	Gly	His	Ile	Cys	Pro	His	Leu	Thr	Pro	Arg	Cys	Leu					
			670						675			680								
cag	cta	atc	ctg	gct	gtg	ctc	agc	cct	gtg	aca	aac	gag	gat	gag	gat	2115				
Gln	Leu	Ile	Leu	Ala	Val	Leu	Ser	Pro	Val	Thr	Asn	Glu	Asp	Glu	Asp					
			685						690			695			700					
gac	aac	gtg	gtg	gtc	act	gat	gac	gct	gat	gag	aag	cag	ctg	cag	cat	2163				
Asp	Asn	Val	Val	Val	Thr	Asp	Asp	Ala	Asp	Glu	Lys	Gln	Leu	Gln	His					
			705						710			715								
gga	gag	gac	gaa	gac	tca	gat	aat	gag	gac	aat	aag	aac	tca	gag	agt	2211				
Gly	Glu	Asp	Glu	Asp	Ser	Asp	Asn	Glu	Asp	Asn	Lys	Asn	Ser	Glu	Ser					
			720						725			730								
gac	atg	gac	agt	gag	gat	ggg	gaa	gaa	agt	gaa	gag	gag	gac	cgt	gac	2259				
Asp	Met	Asp	Ser	Glu	Asp	Gly	Glu	Glu	Ser	Glu	Glu	Glu	Asp	Arg	Asp					
			735						740			745								
aaa	gat	gtg	gac	cca	ggc	ttc	cgt	caa	cag	ttg	atg	gaa	gtg	tta	aaa	2307				
Lys	Asp	Val	Asp	Pro	Gly	Phe	Arg	Gln	Gln	Leu	Met	Glu	Val	Leu	Lys					
			750						755			760								
gct	ggg	aat	gca	ttg	ggc	gga	gtg	gac	aac	gag	gag	gag	gag	gag	ctt	2355				
Ala	Gly	Asn	Ala	Leu	Gly	Gly	Val	Asp	Asn	Glu	Glu	Glu	Glu	Glu	Leu					
			765						770			775			780					
ggg	gat	gag	gcc	atg	atg	gcc	ctg	gac	cag	aac	ctg	gcc	agc	cta	ttt	2403				
Gly	Asp	Glu	Ala	Met	Met	Ala	Leu	Asp	Gln	Asn	Leu	Ala	Ser	Leu	Phe					

785										790					795					
aaa	gag	cag	aag	atg	cgc	atc	cag	gcc	cgg	aat	gag	gag	aaa	aac	aag		2451			
Lys	Glu	Gln	Lys	Met	Arg	Ile	Gln	Ala	Arg	Asn	Glu	Glu	Lys	Asn	Lys					
			800					805					810							
cta	cag	aag	gag	aag	aag	ctc	cga	cgg	gac	ttc	caa	atc	agg	gca	cta		2499			
Leu	Gln	Lys	Glu	Lys	Lys	Leu	Arg	Arg	Asp	Phe	Gln	Ile	Arg	Ala	Leu					
			815				820					825								
gac	ctg	atc	gag	gtg	ctg	gtg	acc	aag	cag	cct	gag	cac	ccc	ctg	atc		2547			
Asp	Leu	Ile	Glu	Val	Leu	Val	Thr	Lys	Gln	Pro	Glu	His	Pro	Leu	Ile					
	830					835					840									
ctg	gaa	cta	ctt	gag	cca	ctg	ctg	aac	gtg	atc	cag	cac	agc	atg	cgc		2595			
Leu	Glu	Leu	Leu	Glu	Pro	Leu	Leu	Asn	Val	Ile	Gln	His	Ser	Met	Arg					
	845				850				855						860					
agc	aaa	ggc	tcc	acc	aag	cag	gag	cag	gac	ctc	ctg	cac	aag	acc	gcc		2643			
Ser	Lys	Gly	Ser	Thr	Lys	Gln	Glu	Gln	Asp	Leu	Leu	His	Lys	Thr	Ala					
				865					870					875						
cgc	atc	ttc	atg	cac	cac	ctg	tgt	cgt	gcc	cgc	cgc	tac	tgc	cac	gag		2691			
Arg	Ile	Phe	Met	His	His	Leu	Cys	Arg	Ala	Arg	Arg	Tyr	Cys	His	Glu					
			880					885					890							
gtg	ggg	ccg	tgt	gca	gag	gct	ctg	cat	gcc	cag	gtg	gag	agg	ctt	gtg		2739			
Val	Gly	Pro	Cys	Ala	Glu	Ala	Leu	His	Ala	Gln	Val	Glu	Arg	Leu	Val					
		895					900					905								
cag	cag	gct	ggc	agc	cag	gct	gat	gcc	tct	gtc	gcc	cta	tac	tat	ttc		2787			
Gln	Gln	Ala	Gly	Ser	Gln	Ala	Asp	Ala	Ser	Val	Ala	Leu	Tyr	Tyr	Phe					
	910					915					920									
aat	gcc	tct	ctg	tac	ctg	ctg	cga	gtc	ctc	aag	ggc	aac	acc	aat	aag		2835			
Asn	Ala	Ser	Leu	Tyr	Leu	Leu	Arg	Val	Leu	Lys	Gly	Asn	Thr	Asn	Lys					
	925					930				935					940					
agg	cac	caa	gat	ggc	cat	aag	tta	cac	gga	gct	gac	aca	gag	gac	tca		2883			
Arg	His	Gln	Asp	Gly	His	Lys	Leu	His	Gly	Ala	Asp	Thr	Glu	Asp	Ser					
				945					950					955						
gag	gac	cag	gct	gct	aac	tgc	tta	gac	ttg	gac	ttt	gtg	acc	cgg	gtg		2931			
Glu	Asp	Gln	Ala	Ala	Asn	Cys	Leu	Asp	Leu	Asp	Phe	Val	Thr	Arg	Val					
			960					965					970							
tat	tca	gca	tca	ctg	gaa	tct	ctt	ctg	acc	aag	cgt	aac	agc	tca	ctt		2979			
Tyr	Ser	Ala	Ser	Leu	Glu	Ser	Leu	Leu	Thr	Lys	Arg	Asn	Ser	Ser	Leu					
			975				980					985								
acg	gtc	ccc	atg	ttc	ctc	agc	ctc	ttc	tcc	aga	tac	cca	gtg	atc	tgt		3027			
Thr	Val	Pro	Met	Phe	Leu	Ser	Leu	Phe	Ser	Arg	Tyr	Pro	Val	Ile	Cys					
	990					995					1000									
aag	aac	ctg	ctt	ccc	gtc	ctg	gct	cag	cat	gtg	gct	ggc	cca	tct			3072			
Lys	Asn	Leu	Leu	Pro	Val	Leu	Ala	Gln	His	Val	Ala	Gly	Pro	Ser						
	1005				1010					1015										
cgg	ccc	cgc	cat	cag	gcc	cag	gca	tgc	ctg	atg	ctc	cag	aag	act			3117			
Arg	Pro	Arg	His	Gln	Ala	Gln	Ala	Cys	Leu	Met	Leu	Gln	Lys	Thr						

1020		1025		1030											
ctg	tct	gca	cga	gag	ctg	aga	gtc	tgt	ttt	gag	gat	cct	gag	tgg	3162
Leu	Ser	Ala	Arg	Glu	Leu	Arg	Val	Cys	Phe	Glu	Asp	Pro	Glu	Trp	
1035					1040					1045					
gag	cag	ctg	att	acc	caa	ctc	ttg	gga	aag	gcc	acc	cag	acc	ctg	3207
Glu	Gln	Leu	Ile	Thr	Gln	Leu	Leu	Gly	Lys	Ala	Thr	Gln	Thr	Leu	
1050					1055					1060					
cag	act	ctt	ggg	gag	gca	cag	agc	aag	ggg	gag	cac	cag	aag	gag	3252
Gln	Thr	Leu	Gly	Glu	Ala	Gln	Ser	Lys	Gly	Glu	His	Gln	Lys	Glu	
1065					1070					1075					
cta	tcc	atc	ttg	gag	ctg	ctg	aac	act	ctg	ttg	agg	aca	gtc	aat	3297
Leu	Ser	Ile	Leu	Glu	Leu	Leu	Asn	Thr	Leu	Leu	Arg	Thr	Val	Asn	
1080					1085					1090					
cac	gag	aag	ctg	tct	gtg	gac	ctc	act	gct	ccc	ttg	ggc	gtg	ctt	3342
His	Glu	Lys	Leu	Ser	Val	Asp	Leu	Thr	Ala	Pro	Leu	Gly	Val	Leu	
1095					1100					1105					
cag	agc	aag	caa	cag	aag	ctg	cag	caa	agc	ctg	cag	cag	ggg	aat	3387
Gln	Ser	Lys	Gln	Gln	Lys	Leu	Gln	Gln	Ser	Leu	Gln	Gln	Gly	Asn	
1110					1115					1120					
cac	tca	tct	ggc	tcc	aat	cgc	ctc	tat	gat	ctc	tac	tgg	cag	gcc	3432
His	Ser	Ser	Gly	Ser	Asn	Arg	Leu	Tyr	Asp	Leu	Tyr	Trp	Gln	Ala	
1125					1130					1135					
atg	agg	atg	cta	gga	gtc	caa	cgt	cca	aag	tca	gaa	aag	aag	aat	3477
Met	Arg	Met	Leu	Gly	Val	Gln	Arg	Pro	Lys	Ser	Glu	Lys	Lys	Asn	
1140					1145					1150					
gcc	aag	gat	att	cct	agt	gac	acc	cag	agc	ccc	gtc	agc	aca	aag	3522
Ala	Lys	Asp	Ile	Pro	Ser	Asp	Thr	Gln	Ser	Pro	Val	Ser	Thr	Lys	
1155					1160					1165					
cgg	aag	aaa	aag	gga	ttc	ttg	cca	gag	acc	aag	aag	cga	aag	aaa	3567
Arg	Lys	Lys	Lys	Gly	Phe	Leu	Pro	Glu	Thr	Lys	Lys	Arg	Lys	Lys	
1170					1175					1180					
ctt	aaa	tct	gag	ggc	acc	aca	cca	gaa	aag	aat	gct	gcg	tca	cag	3612
Leu	Lys	Ser	Glu	Gly	Thr	Thr	Pro	Glu	Lys	Asn	Ala	Ala	Ser	Gln	
1185					1190					1195					
cag	gat	gca	gtg	aca	gag	ggg	gcc	atg	cct	gct	gcc	act	ggg	aaa	3657
Gln	Asp	Ala	Val	Thr	Glu	Gly	Ala	Met	Pro	Ala	Ala	Thr	Gly	Lys	
1200					1205					1210					
gac	cag	ccc	ccc	agc	aca	ggc	aag	aag	aaa	agg	aag	agg	gta	aag	3702
Asp	Gln	Pro	Pro	Ser	Thr	Gly	Lys	Lys	Lys	Arg	Lys	Arg	Val	Lys	
1215					1220					1225					
gcc	agc	acc	cca	tcc	cag	gtg	aat	ggg	ata	act	ggg	gcc	aag	agt	3747
Ala	Ser	Thr	Pro	Ser	Gln	Val	Asn	Gly	Ile	Thr	Gly	Ala	Lys	Ser	
1230					1235					1240					
cca	gct	ccc	agt	aac	ccc	acc	cta	agc	ccc	agc	acc	cct	gcc	aag	3792
Pro	Ala	Pro	Ser	Asn	Pro	Thr	Leu	Ser	Pro	Ser	Thr	Pro	Ala	Lys	

1245		1250		1255	
acc cca aaa ctg cag aag	aaa aaa gag aag ctg	tca cag gtg aat	3837		
Thr Pro Lys Leu Gln Lys	Lys Lys Glu Lys Leu	Ser Gln Val Asn			
1260	1265	1270			
gga gcc act cct gtg tcc	ccc ata gag cct gaa	agc aaa aag cat	3882		
Gly Ala Thr Pro Val Ser	Pro Ile Glu Pro Glu	Ser Lys Lys His			
1275	1280	1285			
cat cag gag gca ctc agc	aca aag gag gtc ata	aga aag tcc ccc	3927		
His Gln Glu Ala Leu Ser	Thr Lys Glu Val Ile	Arg Lys Ser Pro			
1290	1295	1300			
cac ccc cag tct gcc ctg	cca aag aaa aga gca	agg ctg tct ctg	3972		
His Pro Gln Ser Ala Leu	Pro Lys Lys Arg Ala	Arg Leu Ser Leu			
1305	1310	1315			
gtg agc agg agc ccc agc	ctg tta cag agt ggg	gtc aag aaa agg	4017		
Val Ser Arg Ser Pro Ser	Leu Leu Gln Ser Gly	Val Lys Lys Arg			
1320	1325	1330			
aga gtg gcc agc agg aga	gtg cag aca cct tga	gtgtgtatag	4060		
Arg Val Ala Ser Arg Arg	Val Gln Thr Pro				
1335	1340				
tctgtttccc tgcctagag actcctat	tttccaccaat attttaataa	acaatccatg	4120		
atgcta			4126		

<210> 8
 <211> 1344
 <212> PRT
 <213> Mouse

<400> 8

Met Ala Glu Met Lys Ser Pro Thr Lys Ala Glu Pro Ala Thr Pro Ala
1 5 10 15

Glu Ala Ala Gln Ser Asp Arg His Ser Leu Leu Glu His Ser Arg Glu
20 25 30

Phe Leu Asp Phe Phe Trp Asp Ile Ala Lys Pro Asp Gln Glu Thr Arg
35 40 45

Leu Arg Ala Thr Glu Lys Leu Leu Glu Tyr Leu Arg Thr Arg Pro Asn
50 55 60

Asp Ser Glu Met Lys Tyr Ala Leu Lys Arg Leu Ile Thr Gly Leu Gly
65 70 75 80

Val Gly Arg Glu Ala Ala Thr Ala Cys Tyr Ser Leu Ala Leu Ala Gln
85 90 95

Leu Leu Gln Ser Phe Glu Asp Ile Pro Leu Cys Asp Ile Leu Asp Gln
 100 105 110

Ile Gln Glu Lys Tyr Ser Leu Gln Ala Met Asn Lys Ala Met Met Arg
 115 120 125

Pro Ser Leu Phe Ala Asn Leu Phe Gly Val Leu Ala Leu Phe Gln Ser
 130 135 140

Gly Arg Leu Val Lys Asp Lys Glu Ala Leu Met Lys Ser Val Gln Leu
 145 150 155 160

Leu Lys Ile Leu Ser Gln His Pro Asn His Leu Gln Gly Gln Pro Ile
 165 170 175

Lys Ala Leu Val Asp Ile Leu Ser Glu Val Pro Glu Ser Met Phe Gln
 180 185 190

Glu Ile Leu Pro Lys Val Leu Lys Gly Asn Met Lys Val Ile Leu Arg
 195 200 205

Ser Pro Lys Tyr Leu Glu Leu Phe Leu Leu Ala Lys Gln Arg Val Pro
 210 215 220

Thr Lys Leu Glu Ser Leu Met Gly Ser Val Asp Leu Phe Ser Glu Asp
 225 230 235 240

Asn Ile Pro Ser Leu Val Asn Ile Leu Lys Val Ala Ala Asn Ser Val
 245 250 255

Lys Lys Glu His Lys Leu Pro Asn Val Ala Leu Asp Leu Leu Arg Leu
 260 265 270

Ala Leu Lys Glu Ser Arg Phe Glu Leu Phe Trp Lys Lys Val Leu Glu
 275 280 285

Glu Gly Leu Leu Lys Asn Pro Ser Trp Thr Ser Ser Tyr Met Cys Phe
 290 295 300

Arg Leu Leu Gly Ala Ser Leu Pro Leu Leu Ser Glu Glu Gln Leu Gln
 305 310 315 320

Leu Val Met Arg Gly Asp Leu Ile Arg His Phe Gly Glu Asn Met Val
 325 330 335

Ile Ser Lys Pro Gln Asn Leu Phe Lys Ile Ile Pro Glu Ile Ser Thr
340 345 350

Tyr Val Gly Thr Phe Leu Glu Gly Cys Gln Asp Asp Pro Lys Arg Gln
355 360 365

Leu Thr Met Met Val Ala Phe Thr Thr Ile Thr Asn Gln Gly Leu Pro
370 375 380

Val Met Pro Thr Phe Trp Arg Val Thr Arg Phe Leu Asn Ala Glu Ala
385 390 395 400

Leu Gln Ser Tyr Val Ala Trp Leu Arg Asp Met Phe Leu Gln Pro Asp
405 410 415

Leu Asn Ser Leu Val Asp Phe Ser Thr Ala Asn Gln Lys Arg Ala Gln
420 425 430

Asp Ala Ser Leu Asn Val Pro Glu Arg Ala Val Phe Arg Leu Arg Lys
435 440 445

Trp Ile Ile His Arg Leu Val Ser Leu Val Asp His Leu His Leu Glu
450 455 460

Lys Asp Glu Ala Val Val Glu Gln Ile Ala Arg Phe Cys Leu Phe His
465 470 475 480

Ala Phe Phe Lys Thr Lys Lys Ala Thr Pro Gln Ile Pro Glu Thr Lys
485 490 495

Gln His Phe Ser Phe Pro Leu Asp Asp Arg Asn Arg Gly Val Phe Val
500 505 510

Ser Ala Phe Phe Ser Leu Leu Gln Thr Leu Ser Val Lys Phe Arg Gln
515 520 525

Thr Pro Asp Leu Ala Glu Asn Gly Lys Pro Trp Thr Tyr Arg Leu Val
530 535 540

Gln Leu Ala Asp Met Leu Leu Asn His Asn Arg Asn Val Thr Ser Val
545 550 555 560

Thr Ser Leu Thr Thr Gln Gln Arg Gln Ala Trp Asp Gln Met Met Ser
565 570 575

Thr Leu Lys Glu Leu Glu Ala Arg Ser Ser Glu Thr Arg Ala Ile Ala
 580 585 590

Phe Gln His Leu Leu Leu Leu Val Gly Leu His Ile Phe Lys Ser Pro
 595 600 605

Ala Glu Ser Cys Asp Val Leu Gly Asp Ile Gln Thr Cys Ile Lys Lys
 610 615 620

Ser Met Glu Gln Asn Pro Arg Arg Ser Arg Ser Arg Ala Lys Ala Ser
 625 630 635 640

Gln Glu Pro Val Trp Val Glu Val Met Val Glu Ile Leu Leu Ser Leu
 645 650 655

Leu Ala Gln Pro Ser Asn Leu Met Arg Gln Val Val Arg Ser Val Phe
 660 665 670

Gly His Ile Cys Pro His Leu Thr Pro Arg Cys Leu Gln Leu Ile Leu
 675 680 685

Ala Val Leu Ser Pro Val Thr Asn Glu Asp Glu Asp Asp Asn Val Val
 690 695 700

Val Thr Asp Asp Ala Asp Glu Lys Gln Leu Gln His Gly Glu Asp Glu
 705 710 715 720

Asp Ser Asp Asn Glu Asp Asn Lys Asn Ser Glu Ser Asp Met Asp Ser
 725 730 735

Glu Asp Gly Glu Glu Ser Glu Glu Glu Asp Arg Asp Lys Asp Val Asp
 740 745 750

Pro Gly Phe Arg Gln Gln Leu Met Glu Val Leu Lys Ala Gly Asn Ala
 755 760 765

Leu Gly Gly Val Asp Asn Glu Glu Glu Glu Glu Leu Gly Asp Glu Ala
 770 775 780

Met Met Ala Leu Asp Gln Asn Leu Ala Ser Leu Phe Lys Glu Gln Lys
 785 790 795 800

Met Arg Ile Gln Ala Arg Asn Glu Glu Lys Asn Lys Leu Gln Lys Glu
 805 810 815

Lys Lys Leu Arg Arg Asp Phe Gln Ile Arg Ala Leu Asp Leu Ile Glu
820 825 830

Val Leu Val Thr Lys Gln Pro Glu His Pro Leu Ile Leu Glu Leu Leu
835 840 845

Glu Pro Leu Leu Asn Val Ile Gln His Ser Met Arg Ser Lys Gly Ser
850 855 860

Thr Lys Gln Glu Gln Asp Leu Leu His Lys Thr Ala Arg Ile Phe Met
865 870 875 880

His His Leu Cys Arg Ala Arg Arg Tyr Cys His Glu Val Gly Pro Cys
885 890 895

Ala Glu Ala Leu His Ala Gln Val Glu Arg Leu Val Gln Gln Ala Gly
900 905 910

Ser Gln Ala Asp Ala Ser Val Ala Leu Tyr Tyr Phe Asn Ala Ser Leu
915 920 925

Tyr Leu Leu Arg Val Leu Lys Gly Asn Thr Asn Lys Arg His Gln Asp
930 935 940

Gly His Lys Leu His Gly Ala Asp Thr Glu Asp Ser Glu Asp Gln Ala
945 950 955 960

Ala Asn Cys Leu Asp Leu Asp Phe Val Thr Arg Val Tyr Ser Ala Ser
965 970 975

Leu Glu Ser Leu Leu Thr Lys Arg Asn Ser Ser Leu Thr Val Pro Met
980 985 990

Phe Leu Ser Leu Phe Ser Arg Tyr Pro Val Ile Cys Lys Asn Leu Leu
995 1000 1005

Pro Val Leu Ala Gln His Val Ala Gly Pro Ser Arg Pro Arg His
1010 1015 1020

Gln Ala Gln Ala Cys Leu Met Leu Gln Lys Thr Leu Ser Ala Arg
1025 1030 1035

Glu Leu Arg Val Cys Phe Glu Asp Pro Glu Trp Glu Gln Leu Ile
1040 1045 1050

Thr	Gln	Leu	Leu	Gly	Lys	Ala	Thr	Gln	Thr	Leu	Gln	Thr	Leu	Gly
1055						1060					1065			
Glu	Ala	Gln	Ser	Lys	Gly	Glu	His	Gln	Lys	Glu	Leu	Ser	Ile	Leu
1070						1075					1080			
Glu	Leu	Leu	Asn	Thr	Leu	Leu	Arg	Thr	Val	Asn	His	Glu	Lys	Leu
1085						1090					1095			
Ser	Val	Asp	Leu	Thr	Ala	Pro	Leu	Gly	Val	Leu	Gln	Ser	Lys	Gln
1100						1105					1110			
Gln	Lys	Leu	Gln	Gln	Ser	Leu	Gln	Gln	Gly	Asn	His	Ser	Ser	Gly
1115						1120					1125			
Ser	Asn	Arg	Leu	Tyr	Asp	Leu	Tyr	Trp	Gln	Ala	Met	Arg	Met	Leu
1130						1135					1140			
Gly	Val	Gln	Arg	Pro	Lys	Ser	Glu	Lys	Lys	Asn	Ala	Lys	Asp	Ile
1145						1150					1155			
Pro	Ser	Asp	Thr	Gln	Ser	Pro	Val	Ser	Thr	Lys	Arg	Lys	Lys	Lys
1160						1165					1170			
Gly	Phe	Leu	Pro	Glu	Thr	Lys	Lys	Arg	Lys	Lys	Leu	Lys	Ser	Glu
1175						1180					1185			
Gly	Thr	Thr	Pro	Glu	Lys	Asn	Ala	Ala	Ser	Gln	Gln	Asp	Ala	Val
1190						1195					1200			
Thr	Glu	Gly	Ala	Met	Pro	Ala	Ala	Thr	Gly	Lys	Asp	Gln	Pro	Pro
1205						1210					1215			
Ser	Thr	Gly	Lys	Lys	Lys	Arg	Lys	Arg	Val	Lys	Ala	Ser	Thr	Pro
1220						1225					1230			
Ser	Gln	Val	Asn	Gly	Ile	Thr	Gly	Ala	Lys	Ser	Pro	Ala	Pro	Ser
1235						1240					1245			
Asn	Pro	Thr	Leu	Ser	Pro	Ser	Thr	Pro	Ala	Lys	Thr	Pro	Lys	Leu
1250						1255					1260			
Gln	Lys	Lys	Lys	Glu	Lys	Leu	Ser	Gln	Val	Asn	Gly	Ala	Thr	Pro
1265						1270					1275			

Val Ser Pro Ile Glu Pro Glu Ser Lys Lys His His Gln Glu Ala
1280 1285 1290

Leu Ser Thr Lys Glu Val Ile Arg Lys Ser Pro His Pro Gln Ser
1295 1300 1305

Ala Leu Pro Lys Lys Arg Ala Arg Leu Ser Leu Val Ser Arg Ser
1310 1315 1320

Pro Ser Leu Leu Gln Ser Gly Val Lys Lys Arg Arg Val Ala Ser
1325 1330 1335

Arg Arg Val Gln Thr Pro
1340

<210> 9
<211> 2851
<212> DNA
<213> Mouse

<220>
<221> CDS
<222> (76)..(2349)

<400> 9
acgcggggggg aagtgcagcg tgcgtgcggt ttgggtggggtc gctgtgtgctg ctccgcgtgt 60

gcagccgcgt gggcc atg ggg cgg cgg gcg cgg ggc cgg cgg ttc cag cag 111
Met Gly Arg Arg Ala Arg Gly Arg Arg Phe Gln Gln
1 5 10

ccg ccg cag cct gag ggc gag gaa gac gcc agc gac ggc ggc aga aag 159
Pro Pro Gln Pro Glu Gly Glu Glu Asp Ala Ser Asp Gly Gly Arg Lys
15 20 25

cga ggc cag gcg ggc tgg gaa ggt ggc tat ccc gag atc gta aag gag 207
Arg Gly Gln Ala Gly Trp Glu Gly Gly Tyr Pro Glu Ile Val Lys Glu
30 35 40

aac aag ctc ttc gag cac tac tat cag gaa ctc aag atc gtg cca gag 255
Asn Lys Leu Phe Glu His Tyr Tyr Gln Glu Leu Lys Ile Val Pro Glu
45 50 55 60

gga gaa tgg gac caa ttc atg gag tca ctc cga gaa cct ctc cca gcc 303
Gly Glu Trp Asp Gln Phe Met Glu Ser Leu Arg Glu Pro Leu Pro Ala
65 70 75

aca ctg aga atc act ggg tac aaa agc cat gcc aaa gag att ctc cat 351
Thr Leu Arg Ile Thr Gly Tyr Lys Ser His Ala Lys Glu Ile Leu His
80 85 90

tgc ttg aag aac aag tac ttt aag gag ttg gag gac ctg gaa gta gat 399

Cys	Leu	Lys	Asn	Lys	Tyr	Phe	Lys	Glu	Leu	Glu	Asp	Leu	Glu	Val	Asp	
		95					100					105				
gga	cag	aaa	gtt	gaa	gtt	cca	caa	cca	cta	agc	tgg	tac	cct	gaa	gaa	447
Gly	Gln	Lys	Val	Glu	Val	Pro	Gln	Pro	Leu	Ser	Trp	Tyr	Pro	Glu	Glu	
	110					115					120					
ctt	gcc	tgg	cat	aca	aac	tta	agt	cgg	aaa	atc	ttg	agg	aag	tcc	ccg	495
Leu	Ala	Trp	His	Thr	Asn	Leu	Ser	Arg	Lys	Ile	Leu	Arg	Lys	Ser	Pro	
125					130					135					140	
ttg	ttg	gca	aag	ttc	cat	cag	ttc	ctg	gtc	agc	gag	act	gag	tct	gga	543
Leu	Leu	Ala	Lys	Phe	His	Gln	Phe	Leu	Val	Ser	Glu	Thr	Glu	Ser	Gly	
				145					150					155		
aac	atc	agc	cgc	cag	gag	gct	gtc	agc	atg	atc	ccc	cca	ctg	ctg	ctc	591
Asn	Ile	Ser	Arg	Gln	Glu	Ala	Val	Ser	Met	Ile	Pro	Pro	Leu	Leu	Leu	
			160					165					170			
aac	gtg	gag	cca	cac	cat	aag	atc	tta	gac	atg	tgt	gca	gcc	cct	gga	639
Asn	Val	Glu	Pro	His	His	Lys	Ile	Leu	Asp	Met	Cys	Ala	Ala	Pro	Gly	
	175						180					185				
tcc	aag	acc	aca	cag	tta	att	gaa	atg	ttg	cat	gca	gac	atg	agt	gtg	687
Ser	Lys	Thr	Thr	Gln	Leu	Ile	Glu	Met	Leu	His	Ala	Asp	Met	Ser	Val	
	190					195					200					
ccc	ttt	cca	gag	gga	ttt	gta	atc	gca	aat	gac	gtg	gac	aac	aag	cgc	735
Pro	Phe	Pro	Glu	Gly	Phe	Val	Ile	Ala	Asn	Asp	Val	Asp	Asn	Lys	Arg	
205					210					215					220	
tgc	tat	ctg	ctc	gtc	cat	cag	gcc	aaa	agg	ttg	agc	agt	ccc	tgc	atc	783
Cys	Tyr	Leu	Leu	Val	His	Gln	Ala	Lys	Arg	Leu	Ser	Ser	Pro	Cys	Ile	
				225					230					235		
atg	gtg	gta	aac	cat	gac	gca	tcc	agc	ata	cct	aga	ctt	aca	gta	gat	831
Met	Val	Val	Asn	His	Asp	Ala	Ser	Ser	Ile	Pro	Arg	Leu	Thr	Val	Asp	
			240					245					250			
gtg	gac	gga	agg	aaa	gag	att	ctc	ttc	tat	gat	cga	att	tta	tgt	gat	879
Val	Asp	Gly	Arg	Lys	Glu	Ile	Leu	Phe	Tyr	Asp	Arg	Ile	Leu	Cys	Asp	
	255						260					265				
gtc	cct	tgc	agt	ggc	gat	ggc	aca	atg	aga	aaa	aac	att	gat	gtc	tgg	927
Val	Pro	Cys	Ser	Gly	Asp	Gly	Thr	Met	Arg	Lys	Asn	Ile	Asp	Val	Trp	
	270					275					280					
aag	aaa	tgg	aca	acc	tta	aac	agc	ttg	cag	ctc	cat	ggc	ctg	cag	ctt	975
Lys	Lys	Trp	Thr	Thr	Leu	Asn	Ser	Leu	Gln	Leu	His	Gly	Leu	Gln	Leu	
285					290					295					300	
cgg	att	gca	act	cga	ggc	gct	gag	cag	ctg	gcg	gaa	ggc	ggc	agg	atg	1023
Arg	Ile	Ala	Thr	Arg	Gly	Ala	Glu	Gln	Leu	Ala	Glu	Gly	Gly	Arg	Met	
				305					310					315		
gtg	tat	tcc	acg	tgt	tcc	ttg	aac	ccc	gtg	gag	gat	gaa	gca	gtg	atc	1071
Val	Tyr	Ser	Thr	Cys	Ser	Leu	Asn	Pro	Val	Glu	Asp	Glu	Ala	Val	Ile	
			320					325					330			
gca	gct	ctg	cta	gag	aag	agt	gaa	gga	gct	ctt	gag	ctt	gct	gat	gtg	1119

Ala	Ala	Leu	Leu	Glu	Lys	Ser	Glu	Gly	Ala	Leu	Glu	Leu	Ala	Asp	Val	
		335					340					345				
tct	gct	gag	ttg	cca	gga	ctg	aag	tgg	atg	cct	gga	gtc	tca	cag	tgg	1167
Ser	Ala	Glu	Leu	Pro	Gly	Leu	Lys	Trp	Met	Pro	Gly	Val	Ser	Gln	Trp	
		350				355					360					
aag	gtc	atg	act	aga	gac	ggg	cag	tgg	ttt	gca	gac	tgg	cat	gag	gtt	1215
Lys	Val	Met	Thr	Arg	Asp	Gly	Gln	Trp	Phe	Ala	Asp	Trp	His	Glu	Val	
		365			370					375					380	
ccc	cag	ggc	agg	cat	aca	caa	atc	cga	cct	acc	atg	ttc	cca	cca	acg	1263
Pro	Gln	Gly	Arg	His	Thr	Gln	Ile	Arg	Pro	Thr	Met	Phe	Pro	Pro	Thr	
				385					390					395		
gac	ctg	gag	aag	cta	cag	gca	atg	cat	cta	gag	cga	tgc	ctt	cga	atc	1311
Asp	Leu	Glu	Lys	Leu	Gln	Ala	Met	His	Leu	Glu	Arg	Cys	Leu	Arg	Ile	
			400					405					410			
ctg	ccc	cat	cat	cag	aat	act	gga	ggg	ttc	ttt	gtg	gca	gta	ttg	gtc	1359
Leu	Pro	His	His	Gln	Asn	Thr	Gly	Gly	Phe	Phe	Val	Ala	Val	Leu	Val	
		415					420					425				
aag	aaa	gca	cca	atg	ccg	tgg	aac	aaa	cgt	cag	ccc	aag	gtc	cag	aat	1407
Lys	Lys	Ala	Pro	Met	Pro	Trp	Asn	Lys	Arg	Gln	Pro	Lys	Val	Gln	Asn	
		430				435					440					
aaa	tct	gca	gaa	gcc	aga	gaa	ccc	agg	gta	tcc	agc	cat	gtg	gct	gcc	1455
Lys	Ser	Ala	Glu	Ala	Arg	Glu	Pro	Arg	Val	Ser	Ser	His	Val	Ala	Ala	
		445			450					455					460	
aca	gag	gga	aat	ccc	agt	gac	cag	tct	gag	ctg	gaa	agt	cag	atg	ata	1503
Thr	Glu	Gly	Asn	Pro	Ser	Asp	Gln	Ser	Glu	Leu	Glu	Ser	Gln	Met	Ile	
				465					470					475		
act	gga	gct	ggt	gac	tta	gaa	aca	gct	cac	aac	act	gag	aat	aca	gag	1551
Thr	Gly	Ala	Gly	Asp	Leu	Glu	Thr	Ala	His	Asn	Thr	Glu	Asn	Thr	Glu	
			480					485					490			
agc	aat	gag	aag	aaa	gat	ggc	gtg	tgt	ggc	cct	cct	cca	tca	aag	aaa	1599
Ser	Asn	Glu	Lys	Lys	Asp	Gly	Val	Cys	Gly	Pro	Pro	Pro	Ser	Lys	Lys	
		495				500						505				
atg	aag	ttg	ttt	gga	ttt	aaa	gaa	gat	cca	ttt	gta	ttc	att	cct	gaa	1647
Met	Lys	Leu	Phe	Gly	Phe	Lys	Glu	Asp	Pro	Phe	Val	Phe	Ile	Pro	Glu	
		510				515					520					
gat	gat	cct	tta	ttt	cca	cct	att	gag	aag	ttt	tat	gcc	ttg	gat	cct	1695
Asp	Asp	Pro	Leu	Phe	Pro	Pro	Ile	Glu	Lys	Phe	Tyr	Ala	Leu	Asp	Pro	
					530					535					540	
tca	ttc	ccg	agg	atg	aat	ctg	tta	acc	cga	acc	aca	gaa	gga	aag	aag	1743
Ser	Phe	Pro	Arg	Met	Asn	Leu	Leu	Thr	Arg	Thr	Thr	Glu	Gly	Lys	Lys	
				545					550					555		
cgg	cag	ctt	tat	atg	gtc	tcc	aag	gag	ctg	agg	aat	gta	ctg	ctg	aac	1791
Arg	Gln	Leu	Tyr	Met	Val	Ser	Lys	Glu	Leu	Arg	Asn	Val	Leu	Leu	Asn	
			560					565					570			
aac	agc	gag	aag	atg	aag	gtc	att	aac	act	ggg	ata	aaa	gtc	tgg	tgt	1839

Asn	Ser	Glu	Lys	Met	Lys	Val	Ile	Asn	Thr	Gly	Ile	Lys	Val	Trp	Cys	
		575					580					585				
cga	aat	aac	agt	ggg	gaa	gaa	ttc	gat	tgt	gca	ttc	cgt	ttg	gca	cag	1887
Arg	Asn	Asn	Ser	Gly	Glu	Glu	Phe	Asp	Cys	Ala	Phe	Arg	Leu	Ala	Gln	
	590					595					600					
gag	gga	ata	tat	aca	ttg	tat	cca	ttt	atc	aat	tca	aga	atc	atc	act	1935
Glu	Gly	Ile	Tyr	Thr	Leu	Tyr	Pro	Phe	Ile	Asn	Ser	Arg	Ile	Ile	Thr	
605					610					615					620	
gta	tca	atg	gaa	gac	gtg	aag	aca	ctg	ttg	acc	cag	gag	aac	cca	ttc	1983
Val	Ser	Met	Glu	Asp	Val	Lys	Thr	Leu	Leu	Thr	Gln	Glu	Asn	Pro	Phe	
				625					630						635	
ttt	aga	aaa	ctg	agc	agt	gag	gcc	tac	agt	caa	gtc	aag	gac	ctc	gca	2031
Phe	Arg	Lys	Leu	Ser	Ser	Glu	Ala	Tyr	Ser	Gln	Val	Lys	Asp	Leu	Ala	
			640					645						650		
aag	gga	agt	gtt	gtg	ctg	aag	tat	gag	cca	gat	tct	gcg	aat	cca	gac	2079
Lys	Gly	Ser	Val	Val	Leu	Lys	Tyr	Glu	Pro	Asp	Ser	Ala	Asn	Pro	Asp	
		655					660						665			
acc	ctc	cag	tgc	ccc	atc	gtg	ctg	tgt	ggg	tgg	cgg	gga	aag	gcc	tct	2127
Thr	Leu	Gln	Cys	Pro	Ile	Val	Leu	Cys	Gly	Trp	Arg	Gly	Lys	Ala	Ser	
	670					675					680					
att	cga	act	ttt	gtg	ccc	aaa	aat	gag	cgg	ctt	cat	tat	ctc	agg	atg	2175
Ile	Arg	Thr	Phe	Val	Pro	Lys	Asn	Glu	Arg	Leu	His	Tyr	Leu	Arg	Met	
685					690					695					700	
atg	ggg	ctg	gag	gta	ctg	gga	gaa	aag	aag	aaa	gag	gga	gtc	att	ctt	2223
Met	Gly	Leu	Glu	Val	Leu	Gly	Glu	Lys	Lys	Lys	Glu	Gly	Val	Ile	Leu	
				705					710						715	
acc	aat	gag	aat	gct	gcc	agc	cca	gag	cag	cct	gga	gat	gag	gat	gcc	2271
Thr	Asn	Glu	Asn	Ala	Ala	Ser	Pro	Glu	Gln	Pro	Gly	Asp	Glu	Asp	Ala	
			720					725						730		
aag	cag	aca	gca	caa	gac	ccc	tgc	gtc	cca	gac	tcc	gtc	cct	ggc	tgt	2319
Lys	Gln	Thr	Ala	Gln	Asp	Pro	Cys	Val	Pro	Asp	Ser	Val	Pro	Gly	Cys	
		735					740							745		
gat	gca	gct	gca	gct	gag	cca	tcc	cgg	tga	aggagtcttc	acacaatgaa					2369
Asp	Ala	Ala	Ala	Ala	Glu	Pro	Ser	Arg								
	750					755										
ttggtac	cat	ccgttg	ttgg	agatcaa	acc	tagaat	gtcc	ttagcc	aggg	acctg	gaaat					2429
gagtgg	tgcc	cacagt	ctgt	taggagt	cgc	ttttgc	cagag	tgga	tacatg	tttct	gctgt					2489
taaagg	ctaa	cagc	tttgc	agaagt	tcag	atcc	cttgtt	ggcc	agtatt	gacct	agtct					2549
tctaaa	acga	cagta	aaagt	ctaca	agtct	ttggg	aagca	gctct	atcta	tctat	gcttt					2609
aata	ctttct	ggact	gcaca	ccagt	gtgct	gtgc	agtc	at	gctg	acactg	aggt	ctc	agg			2669
tgact	ttctgt	gc	ttt	gtga	t	aaagg	gtga	gata	agccat	ctcag	aggg	agg	ctg	gtga		2729
atcat	gacag	cag	ttt	ggg	gacc	ctt	gt	gctt	atc	ctg	gag	ttg	ttt	aag	tg	2789

gagattgctt gggtcatgaa ataaagagct attatgatca tgaaaaaaaa aaaaaaaaaa 2849

aa 2851

<210> 10
<211> 757
<212> PRT
<213> Mouse

<400> 10

Met Gly Arg Arg Ala Arg Gly Arg Arg Phe Gln Gln Pro Pro Gln Pro
1 5 10 15

Glu Gly Glu Glu Asp Ala Ser Asp Gly Gly Arg Lys Arg Gly Gln Ala
20 25 30

Gly Trp Glu Gly Gly Tyr Pro Glu Ile Val Lys Glu Asn Lys Leu Phe
35 40 45

Glu His Tyr Tyr Gln Glu Leu Lys Ile Val Pro Glu Gly Glu Trp Asp
50 55 60

Gln Phe Met Glu Ser Leu Arg Glu Pro Leu Pro Ala Thr Leu Arg Ile
65 70 75 80

Thr Gly Tyr Lys Ser His Ala Lys Glu Ile Leu His Cys Leu Lys Asn
85 90 95

Lys Tyr Phe Lys Glu Leu Glu Asp Leu Glu Val Asp Gly Gln Lys Val
100 105 110

Glu Val Pro Gln Pro Leu Ser Trp Tyr Pro Glu Glu Leu Ala Trp His
115 120 125

Thr Asn Leu Ser Arg Lys Ile Leu Arg Lys Ser Pro Leu Leu Ala Lys
130 135 140

Phe His Gln Phe Leu Val Ser Glu Thr Glu Ser Gly Asn Ile Ser Arg
145 150 155 160

Gln Glu Ala Val Ser Met Ile Pro Pro Leu Leu Leu Asn Val Glu Pro
165 170 175

His His Lys Ile Leu Asp Met Cys Ala Ala Pro Gly Ser Lys Thr Thr
180 185 190

Gln Leu Ile Glu Met Leu His Ala Asp Met Ser Val Pro Phe Pro Glu
 195 200 205

Gly Phe Val Ile Ala Asn Asp Val Asp Asn Lys Arg Cys Tyr Leu Leu
 210 215 220

Val His Gln Ala Lys Arg Leu Ser Ser Pro Cys Ile Met Val Val Asn
 225 230 235 240

His Asp Ala Ser Ser Ile Pro Arg Leu Thr Val Asp Val Asp Gly Arg
 245 250 255

Lys Glu Ile Leu Phe Tyr Asp Arg Ile Leu Cys Asp Val Pro Cys Ser
 260 265 270

Gly Asp Gly Thr Met Arg Lys Asn Ile Asp Val Trp Lys Lys Trp Thr
 275 280 285

Thr Leu Asn Ser Leu Gln Leu His Gly Leu Gln Leu Arg Ile Ala Thr
 290 295 300

Arg Gly Ala Glu Gln Leu Ala Glu Gly Gly Arg Met Val Tyr Ser Thr
 305 310 315 320

Cys Ser Leu Asn Pro Val Glu Asp Glu Ala Val Ile Ala Ala Leu Leu
 325 330 335

Glu Lys Ser Glu Gly Ala Leu Glu Leu Ala Asp Val Ser Ala Glu Leu
 340 345 350

Pro Gly Leu Lys Trp Met Pro Gly Val Ser Gln Trp Lys Val Met Thr
 355 360 365

Arg Asp Gly Gln Trp Phe Ala Asp Trp His Glu Val Pro Gln Gly Arg
 370 375 380

His Thr Gln Ile Arg Pro Thr Met Phe Pro Pro Thr Asp Leu Glu Lys
 385 390 395 400

Leu Gln Ala Met His Leu Glu Arg Cys Leu Arg Ile Leu Pro His His
 405 410 415

Gln Asn Thr Gly Gly Phe Phe Val Ala Val Leu Val Lys Lys Ala Pro
 420 425 430

Met Pro Trp Asn Lys Arg Gln Pro Lys Val Gln Asn Lys Ser Ala Glu
 435 440 445

Ala Arg Glu Pro Arg Val Ser Ser His Val Ala Ala Thr Glu Gly Asn
 450 455 460

Pro Ser Asp Gln Ser Glu Leu Glu Ser Gln Met Ile Thr Gly Ala Gly
 465 470 475 480

Asp Leu Glu Thr Ala His Asn Thr Glu Asn Thr Glu Ser Asn Glu Lys
 485 490 495

Lys Asp Gly Val Cys Gly Pro Pro Pro Ser Lys Lys Met Lys Leu Phe
 500 505 510

Gly Phe Lys Glu Asp Pro Phe Val Phe Ile Pro Glu Asp Asp Pro Leu
 515 520 525

Phe Pro Pro Ile Glu Lys Phe Tyr Ala Leu Asp Pro Ser Phe Pro Arg
 530 535 540

Met Asn Leu Leu Thr Arg Thr Thr Glu Gly Lys Lys Arg Gln Leu Tyr
 545 550 555 560

Met Val Ser Lys Glu Leu Arg Asn Val Leu Leu Asn Asn Ser Glu Lys
 565 570 575

Met Lys Val Ile Asn Thr Gly Ile Lys Val Trp Cys Arg Asn Asn Ser
 580 585 590

Gly Glu Glu Phe Asp Cys Ala Phe Arg Leu Ala Gln Glu Gly Ile Tyr
 595 600 605

Thr Leu Tyr Pro Phe Ile Asn Ser Arg Ile Ile Thr Val Ser Met Glu
 610 615 620

Asp Val Lys Thr Leu Leu Thr Gln Glu Asn Pro Phe Phe Arg Lys Leu
 625 630 635 640

Ser Ser Glu Ala Tyr Ser Gln Val Lys Asp Leu Ala Lys Gly Ser Val
 645 650 655

Val Leu Lys Tyr Glu Pro Asp Ser Ala Asn Pro Asp Thr Leu Gln Cys
 660 665 670

Pro Ile Val Leu Cys Gly Trp Arg Gly Lys Ala Ser Ile Arg Thr Phe
675 680 685

Val Pro Lys Asn Glu Arg Leu His Tyr Leu Arg Met Met Gly Leu Glu
690 695 700

Val Leu Gly Glu Lys Lys Lys Glu Gly Val Ile Leu Thr Asn Glu Asn
705 710 715 720

Ala Ala Ser Pro Glu Gln Pro Gly Asp Glu Asp Ala Lys Gln Thr Ala
725 730 735

Gln Asp Pro Cys Val Pro Asp Ser Val Pro Gly Cys Asp Ala Ala Ala
740 745 750

Ala Glu Pro Ser Arg
755

<210> 11
<211> 1695
<212> DNA
<213> Mouse

<220>
<221> CDS
<222> (14)..(1234)

<400> 11
acttaaggct gcc atg ggg ccc agt gct cct ctg ctg ctc ctc ttc ttt 49
Met Gly Pro Ser Ala Pro Leu Leu Leu Phe Phe
1 5 10
ttg tca tgg acg gga ccc ctt cag gga cag cag cac cac ctt gtg gag 97
Leu Ser Trp Thr Gly Pro Leu Gln Gly Gln Gln His His Leu Val Glu
15 20 25
tac atg gaa cgc cga cta gct gcc tta gag gaa cgg ctg gcc caa tgc 145
Tyr Met Glu Arg Arg Leu Ala Ala Leu Glu Glu Arg Leu Ala Gln Cys
30 35 40
cag gat cag agt agt cgg cat gct gcc gag ctt cgg gac ttc aaa aac 193
Gln Asp Gln Ser Ser Arg His Ala Ala Glu Leu Arg Asp Phe Lys Asn
45 50 55 60
aag atg ttg cct ctc ctg gag gtg gca gag aag gag cgg gag acc ctc 241
Lys Met Leu Pro Leu Leu Glu Val Ala Glu Lys Glu Arg Glu Thr Leu
65 70 75
aga act gaa gca gac tcc atc tca gga aga gtg gac cgt ctt gaa agg 289
Arg Thr Glu Ala Asp Ser Ile Ser Gly Arg Val Asp Arg Leu Glu Arg
80 85 90

gag gta gac tat ctg gag aca cag aac cca gct ttg ccc tgt gta gag	337
Glu Val Asp Tyr Leu Glu Thr Gln Asn Pro Ala Leu Pro Cys Val Glu	
95 100 105	
ctg gat gag aag gtg act gga ggt cct gga gcc aaa ggc aag ggc cga	385
Leu Asp Glu Lys Val Thr Gly Gly Pro Gly Ala Lys Gly Lys Gly Arg	
110 115 120	
aga aat gag aaa tac gat atg gtg acg gac tgt agc tac aca gtc gct	433
Arg Asn Glu Lys Tyr Asp Met Val Thr Asp Cys Ser Tyr Thr Val Ala	
125 130 135 140	
cag gtg agg tca atg aag atc ctg aag cgg ttt ggt ggt tca gct ggc	481
Gln Val Arg Ser Met Lys Ile Leu Lys Arg Phe Gly Gly Ser Ala Gly	
145 150 155	
cta tgg acc aag gat ccg ctg ggg cca gca gag aag atc tac gtg tta	529
Leu Trp Thr Lys Asp Pro Leu Gly Pro Ala Glu Lys Ile Tyr Val Leu	
160 165 170	
gac ggc acc cag aac gac acg gct ttt gtc ttc cca agg ctg cgt gac	577
Asp Gly Thr Gln Asn Asp Thr Ala Phe Val Phe Pro Arg Leu Arg Asp	
175 180 185	
ttc acc ctt gcc atg gct gcc cgg aaa gct tcc cga att cgg gtg ccc	625
Phe Thr Leu Ala Met Ala Ala Arg Lys Ala Ser Arg Ile Arg Val Pro	
190 195 200	
ttc ccc tgg gta ggc acg ggg cag ctg gtg tac ggt ggc ttc ctt tat	673
Phe Pro Trp Val Gly Thr Gly Gln Leu Val Tyr Gly Gly Phe Leu Tyr	
205 210 215 220	
tat gct cga agg cct cct gga gga cct gga ggg ggt ggt gaa ttg gag	721
Tyr Ala Arg Arg Pro Pro Gly Gly Pro Gly Gly Gly Gly Glu Leu Glu	
225 230 235	
aac act ctg cag ctg atc aaa ttt cac ttg gca aac cga aca gtg gtg	769
Asn Thr Leu Gln Leu Ile Lys Phe His Leu Ala Asn Arg Thr Val Val	
240 245 250	
gat agc tca gtg ttc cct gca gag agc ctg ata ccc ccc tac ggc ctg	817
Asp Ser Ser Val Phe Pro Ala Glu Ser Leu Ile Pro Pro Tyr Gly Leu	
255 260 265	
aca gca gat aca tat atc gac ctg gca gct gat gag gag ggc ctg tgg	865
Thr Ala Asp Thr Tyr Ile Asp Leu Ala Ala Asp Glu Glu Gly Leu Trp	
270 275 280	
gct gtc tat gcc act cga gat gat gac agg cat ttg tgt cta gcc aag	913
Ala Val Tyr Ala Thr Arg Asp Asp Asp Arg His Leu Cys Leu Ala Lys	
285 290 295 300	
tta gac cca cag aca ctt gac aca gag cag cag tgg gac aca cca tgt	961
Leu Asp Pro Gln Thr Leu Asp Thr Glu Gln Gln Trp Asp Thr Pro Cys	
305 310 315	
ccc aga gag aac gca gag gct gcg ttt gtc atc tgt ggg acc ctg tac	1009
Pro Arg Glu Asn Ala Glu Ala Ala Phe Val Ile Cys Gly Thr Leu Tyr	
320 325 330	

gtt gtc tat aac acc cgc cct gcc agt agg gct cgt att cag tgt tcc 1057
 Val Val Tyr Asn Thr Arg Pro Ala Ser Arg Ala Arg Ile Gln Cys Ser
 335 340 345
 ttc gat gcc agt ggt act ctc gcc cct gaa agg gca gca ctc tcc tat 1105
 Phe Asp Ala Ser Gly Thr Leu Ala Pro Glu Arg Ala Ala Leu Ser Tyr
 350 355 360
 ttt cca cgc cga tat ggt gcc cat gcc agc ctt cgc tat aac ccc cgt 1153
 Phe Pro Arg Arg Tyr Gly Ala His Ala Ser Leu Arg Tyr Asn Pro Arg
 365 370 375 380
 gag cgc cag ctg tat gcc tgg gat gat ggc tat cag att gtc tac aaa 1201
 Glu Arg Gln Leu Tyr Ala Trp Asp Asp Gly Tyr Gln Ile Val Tyr Lys
 385 390 395
 ttg gag atg aag aag aag gag gag gaa gtt taa gcagctagcc ttgtgctctt 1254
 Leu Glu Met Lys Lys Lys Glu Glu Glu Val
 400 405
 gattcttatg cccagacatt tatattcctg tgagctctcc tgcagttcat ccttcaaaac 1314
 gaaggccagt ggtggtagct catataccct aatttctaaa ggacaaccaa attctcaagg 1374
 ccctctgttt tatgcagaac tccagatcct gggtagcatt ttagaactga acagcaaaca 1434
 aacaccctaa atcttcactc ctgccctatg tccacaaagt ttagttccaa actcagagcc 1494
 ctgtcctttg gagaggggtca accccagaca gcaggcgaca gcattcttgc cctcagtatg 1554
 accgaaggga gagaactcag agacaaagct gccctccctc ccttccccct ccagtgtagg 1614
 ggagaatggg gctttcccca catcactttg tatggtaaca gtttgcatta aaaggaaaac 1674
 ccacaaaaaa aaaaaaaaaa a 1695

<210> 12
 <211> 406
 <212> PRT
 <213> Mouse

<400> 12

Met Gly Pro Ser Ala Pro Leu Leu Leu Leu Phe Phe Leu Ser Trp Thr
 1 5 10 15
 Gly Pro Leu Gln Gly Gln Gln His His Leu Val Glu Tyr Met Glu Arg
 20 25 30
 Arg Leu Ala Ala Leu Glu Glu Arg Leu Ala Gln Cys Gln Asp Gln Ser
 35 40 45
 Ser Arg His Ala Ala Glu Leu Arg Asp Phe Lys Asn Lys Met Leu Pro
 50 55 60

Leu Leu Glu Val Ala Glu Lys Glu Arg Glu Thr Leu Arg Thr Glu Ala
 65 70 75 80

Asp Ser Ile Ser Gly Arg Val Asp Arg Leu Glu Arg Glu Val Asp Tyr
 85 90 95

Leu Glu Thr Gln Asn Pro Ala Leu Pro Cys Val Glu Leu Asp Glu Lys
 100 105 110

Val Thr Gly Gly Pro Gly Ala Lys Gly Lys Gly Arg Arg Asn Glu Lys
 115 120 125

Tyr Asp Met Val Thr Asp Cys Ser Tyr Thr Val Ala Gln Val Arg Ser
 130 135 140

Met Lys Ile Leu Lys Arg Phe Gly Gly Ser Ala Gly Leu Trp Thr Lys
 145 150 155 160

Asp Pro Leu Gly Pro Ala Glu Lys Ile Tyr Val Leu Asp Gly Thr Gln
 165 170 175

Asn Asp Thr Ala Phe Val Phe Pro Arg Leu Arg Asp Phe Thr Leu Ala
 180 185 190

Met Ala Ala Arg Lys Ala Ser Arg Ile Arg Val Pro Phe Pro Trp Val
 195 200 205

Gly Thr Gly Gln Leu Val Tyr Gly Gly Phe Leu Tyr Tyr Ala Arg Arg
 210 215 220

Pro Pro Gly Gly Pro Gly Gly Gly Gly Glu Leu Glu Asn Thr Leu Gln
 225 230 235 240

Leu Ile Lys Phe His Leu Ala Asn Arg Thr Val Val Asp Ser Ser Val
 245 250 255

Phe Pro Ala Glu Ser Leu Ile Pro Pro Tyr Gly Leu Thr Ala Asp Thr
 260 265 270

Tyr Ile Asp Leu Ala Ala Asp Glu Glu Gly Leu Trp Ala Val Tyr Ala
 275 280 285

Thr Arg Asp Asp Asp Arg His Leu Cys Leu Ala Lys Leu Asp Pro Gln
 290 295 300

Thr Leu Asp Thr Glu Gln Gln Trp Asp Thr Pro Cys Pro Arg Glu Asn
305 310 315 320

Ala Glu Ala Ala Phe Val Ile Cys Gly Thr Leu Tyr Val Val Tyr Asn
325 330 335

Thr Arg Pro Ala Ser Arg Ala Arg Ile Gln Cys Ser Phe Asp Ala Ser
340 345 350

Gly Thr Leu Ala Pro Glu Arg Ala Ala Leu Ser Tyr Phe Pro Arg Arg
355 360 365

Tyr Gly Ala His Ala Ser Leu Arg Tyr Asn Pro Arg Glu Arg Gln Leu
370 375 380

Tyr Ala Trp Asp Asp Gly Tyr Gln Ile Val Tyr Lys Leu Glu Met Lys
385 390 395 400

Lys Lys Glu Glu Glu Val
405

<210> 13
<211> 1610
<212> DNA
<213> Mouse

<220>
<221> CDS
<222> (48)..(1193)

<400> 13
gctgggtact aggagaagcc atcatgcaca cctctactga agccagg atg ggc atg 56
Met Gly Met
1

agg gcg gca ctg aca ggc ttt gcg gtc ctg atg ctg ctc cag agc tgc 104
Arg Ala Ala Leu Thr Gly Phe Ala Val Leu Met Leu Leu Gln Ser Cys
5 10 15

tct gcg tac aag ctg gtc tgc tac ttc acc agc tgg tcc cag tac cgg 152
Ser Ala Tyr Lys Leu Val Cys Tyr Phe Thr Ser Trp Ser Gln Tyr Arg
20 25 30 35

gaa ggc gtt gga agc ttc tta cca gac gcc atc caa cct ttc ctg tgc 200
Glu Gly Val Gly Ser Phe Leu Pro Asp Ala Ile Gln Pro Phe Leu Cys
40 45 50

acc cac atc atc tac agc ttt gcc aac atc agc agc gac aac atg ctt 248
Thr His Ile Ile Tyr Ser Phe Ala Asn Ile Ser Ser Asp Asn Met Leu
55 60 65

agc aca tgg gag tgg aat gac gag tcg aac tat gac aag ctg aat aaa 296

Ser	Thr	Trp	Glu	Trp	Asn	Asp	Glu	Ser	Asn	Tyr	Asp	Lys	Leu	Asn	Lys	
		70					75					80				
ctg	aag	acc	aga	aac	acc	aac	ctg	aag	acc	ctc	ctg	tct	gtt	gga	ggg	344
Leu	Lys	Thr	Arg	Asn	Thr	Asn	Leu	Lys	Thr	Leu	Leu	Ser	Val	Gly	Gly	
	85					90					95					
tgg	aaa	ttt	ggc	gaa	aaa	aga	ttt	tcc	gag	att	gcc	tcc	aac	act	gag	392
Trp	Lys	Phe	Gly	Glu	Lys	Arg	Phe	Ser	Glu	Ile	Ala	Ser	Asn	Thr	Glu	
100					105					110					115	
aga	cgc	act	gct	ttc	gtc	cgg	tcg	gta	gcc	ccg	ttc	ctg	cgt	tct	tat	440
Arg	Arg	Thr	Ala	Phe	Val	Arg	Ser	Val	Ala	Pro	Phe	Leu	Arg	Ser	Tyr	
				120					125						130	
ggc	ttt	gat	ggg	ctg	gat	ctc	gcc	tgg	ctc	tac	cct	cgc	tta	aga	gac	488
Gly	Phe	Asp	Gly	Leu	Asp	Leu	Ala	Trp	Leu	Tyr	Pro	Arg	Leu	Arg	Asp	
			135					140					145			
aag	cag	tat	ttc	tcc	acc	ctg	atc	aag	gaa	ctg	aat	gcg	gaa	ttc	aca	536
Lys	Gln	Tyr	Phe	Ser	Thr	Leu	Ile	Lys	Glu	Leu	Asn	Ala	Glu	Phe	Thr	
		150					155					160				
aag	gag	gtc	cag	cca	ggc	aga	gag	aaa	ctc	ctg	ctc	agc	gca	gct	ttg	584
Lys	Glu	Val	Gln	Pro	Gly	Arg	Glu	Lys	Leu	Leu	Leu	Ser	Ala	Ala	Leu	
	165					170					175					
tca	gca	gga	aag	gtg	gcc	att	gac	act	ggc	tat	gac	atc	gcc	cag	ata	632
Ser	Ala	Gly	Lys	Val	Ala	Ile	Asp	Thr	Gly	Tyr	Asp	Ile	Ala	Gln	Ile	
180					185					190					195	
gcc	caa	cac	ctg	gat	ttt	atc	aat	ctc	atg	acc	tac	gat	ttc	cat	gga	680
Ala	Gln	His	Leu	Asp	Phe	Ile	Asn	Leu	Met	Thr	Tyr	Asp	Phe	His	Gly	
				200					205					210		
gtc	tgg	cgc	caa	atc	aca	ggc	cat	cac	agc	ccc	ctc	ttc	caa	ggc	cag	728
Val	Trp	Arg	Gln	Ile	Thr	Gly	His	His	Ser	Pro	Leu	Phe	Gln	Gly	Gln	
			215					220					225			
aag	gac	act	agg	ttt	gac	aga	tac	agc	aat	gtg	aac	tat	gcc	gtg	cag	776
Lys	Asp	Thr	Arg	Phe	Asp	Arg	Tyr	Ser	Asn	Val	Asn	Tyr	Ala	Val	Gln	
		230					235					240				
tac	atg	ata	cgt	ctg	gga	gcc	cag	gcc	agc	aag	cta	ctg	atg	ggc	atc	824
Tyr	Met	Ile	Arg	Leu	Gly	Ala	Gln	Ala	Ser	Lys	Leu	Leu	Met	Gly	Ile	
	245					250					255					
ccc	acc	ttt	ggg	aag	agc	ttc	act	ctg	gca	tct	tct	gaa	aat	cag	ttg	872
Pro	Thr	Phe	Gly	Lys	Ser	Phe	Thr	Leu	Ala	Ser	Ser	Glu	Asn	Gln	Leu	
260					265					270					275	
gga	gct	cca	atc	tca	ggg	gaa	gga	tta	cca	ggc	cgg	ttc	acc	aag	gag	920
Gly	Ala	Pro	Ile	Ser	Gly	Glu	Gly	Leu	Pro	Gly	Arg	Phe	Thr	Lys	Glu	
				280					285					290		
gca	ggg	acc	ctg	gcc	tac	tac	gag	ata	tgc	gac	ttc	ctc	aaa	gga	gct	968
Ala	Gly	Thr	Leu	Ala	Tyr	Tyr	Glu	Ile	Cys	Asp	Phe	Leu	Lys	Gly	Ala	
			295				300						305			
gaa	gta	cat	cga	ctc	tcc	aac	gag	aag	gtt	ccc	ttc	gct	acc	aag	ggc	1016

Glu Val His Arg Leu Ser Asn Glu Lys Val Pro Phe Ala Thr Lys Gly	
310 315 320	
aac cag tgg gtg ggg tat gag gac aag gag agt gtc aaa aac aag gtt	1064
Asn Gln Trp Val Gly Tyr Glu Asp Lys Glu Ser Val Lys Asn Lys Val	
325 330 335	
ggg ttc ctg aag gag aag aag ctg gca gga gcc atg gtg tgg gca ctg	1112
Gly Phe Leu Lys Glu Lys Lys Leu Ala Gly Ala Met Val Trp Ala Leu	
340 345 350 355	
gat ttg gat gat ttc cag ggc acc tgt cag ccg aag gaa ttc ttc ccg	1160
Asp Leu Asp Asp Phe Gln Gly Thr Cys Gln Pro Lys Glu Phe Phe Pro	
360 365 370	
ctc acc aac gcc atc aag gat gcc ctg gct tag ctcccccttt cccatatggt	1213
Leu Thr Asn Ala Ile Lys Asp Ala Leu Ala	
375 380	
acccccactc tctggccagg agtttaatatct cttgcaatgt taagtcccc aactgagcct	1273
cagttttctcc ttcccttggc acctgtgtaa ggggccacag caggctcagc tatggagaac	1333
agggaaactag ggtaggacga tgggtgggggtt gtgagagtca cagtgtgagc agatacacia	1393
ccctgttaag gaatgcaaat tctcagactc taacctccct ttaccagcc tgaccaaagg	1453
acaccacttg gatcaagtag gcaaatatct tacaggattg agggaccata ctaattatac	1513
cctctgcaaa gcccaacttg aatccttccc ttaggaactt aatcgtcca cttccctttc	1573
cctaattcca cagctgttca ataaagcgcc agaacct	1610
<210> 14	
<211> 381	
<212> PRT	
<213> Mouse	
<400> 14	
Met Gly Met Arg Ala Ala Leu Thr Gly Phe Ala Val Leu Met Leu Leu	
1 5 10 15	
Gln Ser Cys Ser Ala Tyr Lys Leu Val Cys Tyr Phe Thr Ser Trp Ser	
20 25 30	
Gln Tyr Arg Glu Gly Val Gly Ser Phe Leu Pro Asp Ala Ile Gln Pro	
35 40 45	
Phe Leu Cys Thr His Ile Ile Tyr Ser Phe Ala Asn Ile Ser Ser Asp	
50 55 60	
Asn Met Leu Ser Thr Trp Glu Trp Asn Asp Glu Ser Asn Tyr Asp Lys	
65 70 75 80	

Leu Asn Lys Leu Lys Thr Arg Asn Thr Asn Leu Lys Thr Leu Leu Ser
 85 90 95

Val Gly Gly Trp Lys Phe Gly Glu Lys Arg Phe Ser Glu Ile Ala Ser
 100 105 110

Asn Thr Glu Arg Arg Thr Ala Phe Val Arg Ser Val Ala Pro Phe Leu
 115 120 125

Arg Ser Tyr Gly Phe Asp Gly Leu Asp Leu Ala Trp Leu Tyr Pro Arg
 130 135 140

Leu Arg Asp Lys Gln Tyr Phe Ser Thr Leu Ile Lys Glu Leu Asn Ala
 145 150 155 160

Glu Phe Thr Lys Glu Val Gln Pro Gly Arg Glu Lys Leu Leu Leu Ser
 165 170 175

Ala Ala Leu Ser Ala Gly Lys Val Ala Ile Asp Thr Gly Tyr Asp Ile
 180 185 190

Ala Gln Ile Ala Gln His Leu Asp Phe Ile Asn Leu Met Thr Tyr Asp
 195 200 205

Phe His Gly Val Trp Arg Gln Ile Thr Gly His His Ser Pro Leu Phe
 210 215 220

Gln Gly Gln Lys Asp Thr Arg Phe Asp Arg Tyr Ser Asn Val Asn Tyr
 225 230 235 240

Ala Val Gln Tyr Met Ile Arg Leu Gly Ala Gln Ala Ser Lys Leu Leu
 245 250 255

Met Gly Ile Pro Thr Phe Gly Lys Ser Phe Thr Leu Ala Ser Ser Glu
 260 265 270

Asn Gln Leu Gly Ala Pro Ile Ser Gly Glu Gly Leu Pro Gly Arg Phe
 275 280 285

Thr Lys Glu Ala Gly Thr Leu Ala Tyr Tyr Glu Ile Cys Asp Phe Leu
 290 295 300

Lys Gly Ala Glu Val His Arg Leu Ser Asn Glu Lys Val Pro Phe Ala
 305 310 315 320

Thr Lys Gly Asn Gln Trp Val Gly Tyr Glu Asp Lys Glu Ser Val Lys
325 330 335

Asn Lys Val Gly Phe Leu Lys Glu Lys Lys Leu Ala Gly Ala Met Val
340 345 350

Trp Ala Leu Asp Leu Asp Asp Phe Gln Gly Thr Cys Gln Pro Lys Glu
355 360 365

Phe Phe Pro Leu Thr Asn Ala Ile Lys Asp Ala Leu Ala
370 375 380

<210> 15
<211> 2002
<212> DNA
<213> Mouse

<220>
<221> CDS
<222> (178) .. (1689)

<400> 15
gaattccgga aggggggctct gaccggttcc gagcgccaac gcagcctctg tagcccgcaa 60
gtcttcgctcg cttgctccgg gctctgaagt ccggggccac caggggccgc agcgctgggg 120
ggtcgggtcta gctgcgagga tccgggctgc ccacgaagcg aaggcggggc gcccagg 177
atg gga tgc gtg aag tcc agg ttc ctc cga gat gga agc aag gcc tca 225
Met Gly Cys Val Lys Ser Arg Phe Leu Arg Asp Gly Ser Lys Ala Ser
1 5 10 15
aaa aca gag cca agt gcc aat cag aag ggc cct gtg tat gtg ccg gat 273
Lys Thr Glu Pro Ser Ala Asn Gln Lys Gly Pro Val Tyr Val Pro Asp
20 25 30
ccc acg tcc tcc agc aag ctg gga cca aac aac agc aac agc atg ccc 321
Pro Thr Ser Ser Ser Lys Leu Gly Pro Asn Asn Ser Asn Ser Met Pro
35 40 45
cca ggg ttt gtg gag ggc tct gag gat acc att gtg gtc gca ctg tac 369
Pro Gly Phe Val Glu Gly Ser Glu Asp Thr Ile Val Val Ala Leu Tyr
50 55 60
gac tat gag gct att cac cgt gaa gac ctc agc ttc cag aag gga gac 417
Asp Tyr Glu Ala Ile His Arg Glu Asp Leu Ser Phe Gln Lys Gly Asp
65 70 75 80
cag atg gtg gtt ctg gag gag gct ggg gag tgg tgg aag gca cgg tcc 465
Gln Met Val Val Leu Glu Glu Ala Gly Glu Trp Trp Lys Ala Arg Ser
85 90 95
ctg gct acc aag aag gaa ggc tac atc cca agc aac tat gtg gct cga 513
Leu Ala Thr Lys Lys Glu Gly Tyr Ile Pro Ser Asn Tyr Val Ala Arg

	100	105	110	
gtt aac tct ttg gag aca gaa gag tgg ttc ttc aag ggg atc agc cgg	561			
Val Asn Ser Leu Glu Thr Glu Glu Trp Phe Phe Lys Gly Ile Ser Arg				
115 120 125				
aag gat gca gag cgc cac ctc ctg gct cca ggc aac atg ctg ggc tcc	609			
Lys Asp Ala Glu Arg His Leu Leu Ala Pro Gly Asn Met Leu Gly Ser				
130 135 140				
ttc atg atc cgg gac agt gag acc acc aaa ggg agc tac tcg ttg tct	657			
Phe Met Ile Arg Asp Ser Glu Thr Thr Lys Gly Ser Tyr Ser Leu Ser				
145 150 155 160				
gtt cga gac ttt gac ccc cag cac gga gac acc gtg aag cac tat aag	705			
Val Arg Asp Phe Asp Pro Gln His Gly Asp Thr Val Lys His Tyr Lys				
165 170 175				
atc cgg acg ctg gac agt gga ggc ttc tac atc tct cca agg agc acc	753			
Ile Arg Thr Leu Asp Ser Gly Gly Phe Tyr Ile Ser Pro Arg Ser Thr				
180 185 190				
ttc agc agc ctg cag gaa ctc gtg ctc cac tac aag aag ggg aag gat	801			
Phe Ser Ser Leu Gln Glu Leu Val Leu His Tyr Lys Lys Gly Lys Asp				
195 200 205				
ggg ctc tgc cag aag ctg tca gtg ccc tgt gtg tct ccc aaa ccc cag	849			
Gly Leu Cys Gln Lys Leu Ser Val Pro Cys Val Ser Pro Lys Pro Gln				
210 215 220				
aag cca tgg gag aaa gat gct tgg gag att cct cga gaa tcc ctc cag	897			
Lys Pro Trp Glu Lys Asp Ala Trp Glu Ile Pro Arg Glu Ser Leu Gln				
225 230 235 240				
atg gag aag aaa ctt gga gct ggg cag ttt gga gaa gtg tgg atg gcc	945			
Met Glu Lys Lys Leu Gly Ala Gly Gln Phe Gly Glu Val Trp Met Ala				
245 250 255				
acc tac aac aag cac acc aaa gtg gcg gtg aag aca atg aag cca ggg	993			
Thr Tyr Asn Lys His Thr Lys Val Ala Val Lys Thr Met Lys Pro Gly				
260 265 270				
agc atg tcc gtg gag gcc ttc ctg gct gag gcc aac ctg atg aag tcg	1041			
Ser Met Ser Val Glu Ala Phe Leu Ala Glu Ala Asn Leu Met Lys Ser				
275 280 285				
ctg cag cat gac aaa ctg gtg aag cta cac gct gtg gtc tct cag gag	1089			
Leu Gln His Asp Lys Leu Val Lys Leu His Ala Val Val Ser Gln Glu				
290 295 300				
ccc atc ttt att gtc acg gag ttc atg gcc aaa gga agc ctg ctg gac	1137			
Pro Ile Phe Ile Val Thr Glu Phe Met Ala Lys Gly Ser Leu Leu Asp				
305 310 315 320				
ttt ctc aag agt gaa gaa ggc agc aag cag cca ctg cca aaa ctc att	1185			
Phe Leu Lys Ser Glu Glu Gly Ser Lys Gln Pro Leu Pro Lys Leu Ile				
325 330 335				
gac ttc tca gcc cag atc tca gaa ggc atg gcc ttc att gag cag agg	1233			
Asp Phe Ser Ala Gln Ile Ser Glu Gly Met Ala Phe Ile Glu Gln Arg				

340	345	350	
aac tac atc cac cga gac ctg agg gct gcc aac atc tta gtc tct gca			1281
Asn Tyr Ile His Arg Asp Leu Arg Ala Ala Asn Ile Leu Val Ser Ala			
355	360	365	
tca ctg gtg tgt aag att gct gac ttt gga ctg gca cga atc atc gag			1329
Ser Leu Val Cys Lys Ile Ala Asp Phe Gly Leu Ala Arg Ile Ile Glu			
370	375	380	
gac aat gag tac aca gct cgg gaa gga gcc aag ttc ccc atc aag tgg			1377
Asp Asn Glu Tyr Thr Ala Arg Glu Gly Ala Lys Phe Pro Ile Lys Trp			
385	390	395	400
aca gct cct gaa gcc atc aac ttt ggt tcc ttc acc atc aag tca gat			1425
Thr Ala Pro Glu Ala Ile Asn Phe Gly Ser Phe Thr Ile Lys Ser Asp			
	405	410	415
gtc tgg tcc ttt ggt atc ctg ctg atg gaa att gtc acc tat ggc cgg			1473
Val Trp Ser Phe Gly Ile Leu Leu Met Glu Ile Val Thr Tyr Gly Arg			
	420	425	430
atc cct tac cca ggt atg tca aac cca gag gtg att cgg gca cta gag			1521
Ile Pro Tyr Pro Gly Met Ser Asn Pro Glu Val Ile Arg Ala Leu Glu			
	435	440	445
cat ggg tac cgt atg cct cga cca gat aac tgt cca gaa gag ctc tac			1569
His Gly Tyr Arg Met Pro Arg Pro Asp Asn Cys Pro Glu Glu Leu Tyr			
	450	455	460
aat atc atg atc cgc tgc tgg aag aac cgc ccc gag gaa cgg ccc acc			1617
Asn Ile Met Ile Arg Cys Trp Lys Asn Arg Pro Glu Glu Arg Pro Thr			
465	470	475	480
ttt gaa tac atc cag agt gtg ctg gat gac ttc tac acg gcc act gag			1665
Phe Glu Tyr Ile Gln Ser Val Leu Asp Asp Phe Tyr Thr Ala Thr Glu			
	485	490	495
agc cag tat cag cag cag cct tga cagcagtaag gacatgagca gagccagaag			1719
Ser Gln Tyr Gln Gln Gln Pro			
500			
ccccatcagt gccttgacac gcccaacttg ctgggcccac tctcagacac cacaccacac			1779
acactgcagc tggttgagtgg gtgggaggac ttcacaatct ctttctgact ctagtcatct			1839
gcaatccgcc actctcaggg cctccaagtt ggtatgtctc atttgcttgg aatgactgaa			1899
ttcaatctat agctgtgatt taagtggaaa ctgttagaat agtatTTaaa taaaagatat			1959
gaatgtcaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa			2002
<210> 16			
<211> 503			
<212> PRT			
<213> Mouse			
<400> 16			

Met	Gly	Cys	Val	Lys	Ser	Arg	Phe	Leu	Arg	Asp	Gly	Ser	Lys	Ala	Ser	1	5	10	15
Lys	Thr	Glu	Pro	Ser	Ala	Asn	Gln	Lys	Gly	Pro	Val	Tyr	Val	Pro	Asp	20	25	30	
Pro	Thr	Ser	Ser	Ser	Lys	Leu	Gly	Pro	Asn	Asn	Ser	Asn	Ser	Met	Pro	35	40	45	
Pro	Gly	Phe	Val	Glu	Gly	Ser	Glu	Asp	Thr	Ile	Val	Val	Ala	Leu	Tyr	50	55	60	
Asp	Tyr	Glu	Ala	Ile	His	Arg	Glu	Asp	Leu	Ser	Phe	Gln	Lys	Gly	Asp	65	70	75	80
Gln	Met	Val	Val	Leu	Glu	Glu	Ala	Gly	Glu	Trp	Trp	Lys	Ala	Arg	Ser	85	90	95	
Leu	Ala	Thr	Lys	Lys	Glu	Gly	Tyr	Ile	Pro	Ser	Asn	Tyr	Val	Ala	Arg	100	105	110	
Val	Asn	Ser	Leu	Glu	Thr	Glu	Glu	Trp	Phe	Phe	Lys	Gly	Ile	Ser	Arg	115	120	125	
Lys	Asp	Ala	Glu	Arg	His	Leu	Leu	Ala	Pro	Gly	Asn	Met	Leu	Gly	Ser	130	135	140	
Phe	Met	Ile	Arg	Asp	Ser	Glu	Thr	Thr	Lys	Gly	Ser	Tyr	Ser	Leu	Ser	145	150	155	160
Val	Arg	Asp	Phe	Asp	Pro	Gln	His	Gly	Asp	Thr	Val	Lys	His	Tyr	Lys	165	170	175	
Ile	Arg	Thr	Leu	Asp	Ser	Gly	Gly	Phe	Tyr	Ile	Ser	Pro	Arg	Ser	Thr	180	185	190	
Phe	Ser	Ser	Leu	Gln	Glu	Leu	Val	Leu	His	Tyr	Lys	Lys	Gly	Lys	Asp	195	200	205	
Gly	Leu	Cys	Gln	Lys	Leu	Ser	Val	Pro	Cys	Val	Ser	Pro	Lys	Pro	Gln	210	215	220	
Lys	Pro	Trp	Glu	Lys	Asp	Ala	Trp	Glu	Ile	Pro	Arg	Glu	Ser	Leu	Gln	225	230	235	240

Met Glu Lys Lys Leu Gly Ala Gly Gln Phe Gly Glu Val Trp Met Ala
 245 250 255
 Thr Tyr Asn Lys His Thr Lys Val Ala Val Lys Thr Met Lys Pro Gly
 260 265 270
 Ser Met Ser Val Glu Ala Phe Leu Ala Glu Ala Asn Leu Met Lys Ser
 275 280 285
 Leu Gln His Asp Lys Leu Val Lys Leu His Ala Val Val Ser Gln Glu
 290 295 300
 Pro Ile Phe Ile Val Thr Glu Phe Met Ala Lys Gly Ser Leu Leu Asp
 305 310 315 320
 Phe Leu Lys Ser Glu Glu Gly Ser Lys Gln Pro Leu Pro Lys Leu Ile
 325 330 335
 Asp Phe Ser Ala Gln Ile Ser Glu Gly Met Ala Phe Ile Glu Gln Arg
 340 345 350
 Asn Tyr Ile His Arg Asp Leu Arg Ala Ala Asn Ile Leu Val Ser Ala
 355 360 365
 Ser Leu Val Cys Lys Ile Ala Asp Phe Gly Leu Ala Arg Ile Ile Glu
 370 375 380
 Asp Asn Glu Tyr Thr Ala Arg Glu Gly Ala Lys Phe Pro Ile Lys Trp
 385 390 395 400
 Thr Ala Pro Glu Ala Ile Asn Phe Gly Ser Phe Thr Ile Lys Ser Asp
 405 410 415
 Val Trp Ser Phe Gly Ile Leu Leu Met Glu Ile Val Thr Tyr Gly Arg
 420 425 430
 Ile Pro Tyr Pro Gly Met Ser Asn Pro Glu Val Ile Arg Ala Leu Glu
 435 440 445
 His Gly Tyr Arg Met Pro Arg Pro Asp Asn Cys Pro Glu Glu Leu Tyr
 450 455 460
 Asn Ile Met Ile Arg Cys Trp Lys Asn Arg Pro Glu Glu Arg Pro Thr
 465 470 475 480

Phe Glu Tyr Ile Gln Ser Val Leu Asp Asp Phe Tyr Thr Ala Thr Glu
485 490 495

Ser Gln Tyr Gln Gln Gln Pro
500

<210> 17
<211> 3064
<212> DNA
<213> Mouse

<220>
<221> CDS
<222> (133) .. (2463)

<400> 17
ctcacttttgc ccgggtcccg ggaggccgctc gacttatcct aggagctcgg agctttttctt 60
ctgggcaacc agggcgcttc cagacagagt tcctgctgcc acccaccacc cccctctcag 120
cacaggacaa gg atg gag ctc cat ttt ggc tcc tgc ctc tcc ggc tgt ttg 171
Met Glu Leu His Phe Gly Ser Cys Leu Ser Gly Cys Leu
1 5 10
gct ctg ctt gtc ttg ctg cct tcc ctg agc cta gca cag tac gag ggc 219
Ala Leu Leu Val Leu Leu Pro Ser Leu Ser Leu Ala Gln Tyr Glu Gly
15 20 25
tgg ccc tac cag ctc cag tac cct gag tac ttc cag cag ccc gct cct 267
Trp Pro Tyr Gln Leu Gln Tyr Pro Glu Tyr Phe Gln Gln Pro Ala Pro
30 35 40 45
gag cac cat cag cgg cag gtg ccc tcc gat gtg gtc aag atc cag gtc 315
Glu His His Gln Arg Gln Val Pro Ser Asp Val Val Lys Ile Gln Val
50 55 60
cgc ctg gcg ggc cag aag agg aag cac aat gag ggc cgc gtg gag gtc 363
Arg Leu Ala Gly Gln Lys Arg Lys His Asn Glu Gly Arg Val Glu Val
65 70 75
tac tac gaa ggc cag tgg ggc acg gtg tgc gac gat gac ttc tcg atc 411
Tyr Tyr Glu Gly Gln Trp Gly Thr Val Cys Asp Asp Asp Phe Ser Ile
80 85 90
cat gcc gcc cat gtg gtc tgc cgg caa gtg ggc tat gta gag gcc aag 459
His Ala Ala His Val Val Cys Arg Gln Val Gly Tyr Val Glu Ala Lys
95 100 105
tcc tgg gct gcc agc tcc tcc tac ggt cca ggc gaa ggc ccc atc tgg 507
Ser Trp Ala Ala Ser Ser Ser Tyr Gly Pro Gly Glu Gly Pro Ile Trp
110 115 120 125
ttg gac aat atc tac tgt act ggc aaa gag tcg acc ctg gca tct tgc 555
Leu Asp Asn Ile Tyr Cys Thr Gly Lys Glu Ser Thr Leu Ala Ser Cys
130 135 140
tcc tcc aat ggc tgg ggt gtc act gac tgc aag cac act gaa gac gtt 603

Ser	Ser	Asn	Gly	Trp	Gly	Val	Thr	Asp	Cys	Lys	His	Thr	Glu	Asp	Val	
			145					150					155			
gga	gtg	gtg	tgt	agt	gag	aaa	aga	att	cct	ggc	ttc	aaa	ttt	gac	aat	651
Gly	Val	Val	Cys	Ser	Glu	Lys	Arg	Ile	Pro	Gly	Phe	Lys	Phe	Asp	Asn	
			160				165					170				
tcg	ttg	atc	aac	caa	ata	gag	agc	cta	aat	ata	cag	gtg	gaa	gac	atc	699
Ser	Leu	Ile	Asn	Gln	Ile	Glu	Ser	Leu	Asn	Ile	Gln	Val	Glu	Asp	Ile	
			175			180					185					
cgg	att	cgg	ccc	atc	ctt	tct	gcc	ttt	cgc	cat	cgc	aag	cct	gtg	aca	747
Arg	Ile	Arg	Pro	Ile	Leu	Ser	Ala	Phe	Arg	His	Arg	Lys	Pro	Val	Thr	
190					195					200					205	
gag	ggc	tac	gtg	gag	gtg	aag	gag	ggc	aag	gct	tgg	aag	cag	atc	tgc	795
Glu	Gly	Tyr	Val	Glu	Val	Lys	Glu	Gly	Lys	Ala	Trp	Lys	Gln	Ile	Cys	
			210						215				220			
aac	aaa	cac	tgg	aca	gcc	aag	aat	tcc	cac	gtg	gtc	tgt	ggc	atg	ttc	843
Asn	Lys	His	Trp	Thr	Ala	Lys	Asn	Ser	His	Val	Val	Cys	Gly	Met	Phe	
			225					230					235			
ggc	ttc	cct	gca	gag	aag	acc	tac	aac	ccc	aaa	gcc	tat	aaa	acc	ttt	891
Gly	Phe	Pro	Ala	Glu	Lys	Thr	Tyr	Asn	Pro	Lys	Ala	Tyr	Lys	Thr	Phe	
		240					245					250				
gcc	tcg	cgg	agg	aag	ctg	cgt	tac	tgg	aag	ttt	tct	atg	aac	tgc	acg	939
Ala	Ser	Arg	Arg	Lys	Leu	Arg	Tyr	Trp	Lys	Phe	Ser	Met	Asn	Cys	Thr	
	255				260						265					
ggc	act	gaa	gcg	cat	atc	tcc	agc	tgc	aag	ctg	ggc	cct	tcc	gtg	acc	987
Gly	Thr	Glu	Ala	His	Ile	Ser	Ser	Cys	Lys	Leu	Gly	Pro	Ser	Val	Thr	
270					275					280					285	
cgg	gac	cct	gtg	aag	aac	gcc	acc	tgt	gag	aac	ggg	cag	cca	gct	gtg	1035
Arg	Asp	Pro	Val	Lys	Asn	Ala	Thr	Cys	Glu	Asn	Gly	Gln	Pro	Ala	Val	
				290					295				300			
gtc	agt	tgt	gtg	cct	agc	cag	atc	ttc	agc	ccc	gat	gga	ccc	tca	agg	1083
Val	Ser	Cys	Val	Pro	Ser	Gln	Ile	Phe	Ser	Pro	Asp	Gly	Pro	Ser	Arg	
			305					310					315			
ttc	cgg	aaa	gcc	tac	aag	cca	gag	caa	ccc	ttg	gtg	cgc	ctg	aga	ggt	1131
Phe	Arg	Lys	Ala	Tyr	Lys	Pro	Glu	Gln	Pro	Leu	Val	Arg	Leu	Arg	Gly	
		320					325					330				
gga	gcc	cag	gtc	ggg	gag	ggc	cga	gtg	gag	gtg	ctg	aag	aat	gga	gaa	1179
Gly	Ala	Gln	Val	Gly	Glu	Gly	Arg	Val	Glu	Val	Leu	Lys	Asn	Gly	Glu	
	335					340					345					
tgg	gga	acc	atc	tgc	gat	gac	aag	tgg	gac	ctg	gta	tct	gcc	agt	gtg	1227
Trp	Gly	Thr	Ile	Cys	Asp	Asp	Lys	Trp	Asp	Leu	Val	Ser	Ala	Ser	Val	
350					355					360					365	
gtc	tgc	cga	gag	ctg	ggc	ttt	ggg	acc	gct	aaa	gag	gcc	atc	aca	ggc	1275
Val	Cys	Arg	Glu	Leu	Gly	Phe	Gly	Thr	Ala	Lys	Glu	Ala	Ile	Thr	Gly	
				370					375					380		
tcc	aga	cta	ggg	caa	ggg	att	ggg	ccc	atc	cat	ctc	aat	gaa	gtc	cag	1323

Ser	Arg	Leu	Gly	Gln	Gly	Ile	Gly	Pro	Ile	His	Leu	Asn	Glu	Val	Gln		
			385					390					395				
tgc	aca	ggg	act	gag	aag	tcc	atc	ata	gac	tgc	aaa	ttc	aac	aca	gag	1371	
Cys	Thr	Gly	Thr	Glu	Lys	Ser	Ile	Ile	Asp	Cys	Lys	Phe	Asn	Thr	Glu		
		400					405					410					
tct	caa	ggc	tgc	aac	cat	gaa	gaa	gat	gcc	ggg	gtg	cga	tgc	aac	atc	1419	
Ser	Gln	Gly	Cys	Asn	His	Glu	Glu	Asp	Ala	Gly	Val	Arg	Cys	Asn	Ile		
	415					420					425						
ccc	atc	atg	ggg	ttc	cag	aaa	aag	gtg	cgc	ctg	aat	gga	ggc	cgc	aat	1467	
Pro	Ile	Met	Gly	Phe	Gln	Lys	Lys	Val	Arg	Leu	Asn	Gly	Gly	Arg	Asn		
430					435					440					445		
cct	tat	gag	ggc	cga	gtg	gag	gtg	cta	aca	gag	aga	aat	ggg	tcc	ctt	1515	
Pro	Tyr	Glu	Gly	Arg	Val	Glu	Val	Leu	Thr	Glu	Arg	Asn	Gly	Ser	Leu		
				450					455					460			
gtt	tgg	ggg	act	gta	tgc	ggc	cag	aac	tgg	ggc	att	gtg	gaa	gcc	atg	1563	
Val	Trp	Gly	Thr	Val	Cys	Gly	Gln	Asn	Trp	Gly	Ile	Val	Glu	Ala	Met		
		465						470					475				
gtg	gtc	tgc	cgg	cag	cta	ggc	ctg	ggc	ttt	gcc	agc	aat	gcc	ttt	cag	1611	
Val	Val	Cys	Arg	Gln	Leu	Gly	Leu	Gly	Phe	Ala	Ser	Asn	Ala	Phe	Gln		
		480				485						490					
gag	acc	tgg	tac	tgg	cat	gga	aat	atc	ttc	gcc	aac	aac	gtg	gtc	atg	1659	
Glu	Thr	Trp	Tyr	Trp	His	Gly	Asn	Ile	Phe	Ala	Asn	Asn	Val	Val	Met		
	495					500					505						
agt	gga	gtg	aag	tgc	tca	gga	acg	gag	ctg	tcc	cta	gca	cac	tgc	cgc	1707	
Ser	Gly	Val	Lys	Cys	Ser	Gly	Thr	Glu	Leu	Ser	Leu	Ala	His	Cys	Arg		
510					515					520					525		
cat	gac	gag	gag	gtg	gcc	tgc	ccc	gag	ggc	ggg	gtg	cgg	ttt	ggg	gct	1755	
His	Asp	Glu	Glu	Val	Ala	Cys	Pro	Glu	Gly	Gly	Val	Arg	Phe	Gly	Ala		
				530					535					540			
gga	gtc	gcc	tgc	tcg	gaa	act	gca	cct	gac	ctg	gtg	ctt	aat	gct	gag	1803	
Gly	Val	Ala	Cys	Ser	Glu	Thr	Ala	Pro	Asp	Leu	Val	Leu	Asn	Ala	Glu		
		545						550					555				
att	gtc	cag	cag	act	gcc	tac	ctg	gag	gac	agg	ccc	atg	tcc	ttg	ctg	1851	
Ile	Val	Gln	Gln	Thr	Ala	Tyr	Leu	Glu	Asp	Arg	Pro	Met	Ser	Leu	Leu		
		560					565					570					
cag	tgt	gcc	atg	gag	gag	aac	tgc	ctc	tcc	gcc	tcc	gct	gtg	cac	acc	1899	
Gln	Cys	Ala	Met	Glu	Glu	Asn	Cys	Leu	Ser	Ala	Ser	Ala	Val	His	Thr		
	575					580					585						
gac	ccc	acc	aga	ggc	cac	cgg	cgc	ctt	tta	cgc	ttc	tcc	tcc	cag	atc	1947	
Asp	Pro	Thr	Arg	Gly	His	Arg	Arg	Leu	Leu	Arg	Phe	Ser	Ser	Gln	Ile		
590					595					600					605		
cac	aac	aat	ggc	cag	tct	gac	ttc	cgc	ccc	aag	aat	ggc	cgc	cat	gcg	1995	
His	Asn	Asn	Gly	Gln	Ser	Asp	Phe	Arg	Pro	Lys	Asn	Gly	Arg	His	Ala		
			610					615						620			
tgg	att	tgg	cac	gac	tgc	cac	agg	cac	tac	cac	agc	atg	gaa	gtc	ttc	2043	

Trp	Ile	Trp	His	Asp	Cys	His	Arg	His	Tyr	His	Ser	Met	Glu	Val	Phe	
			625					630					635			
act	tac	tat	gac	ctg	ctg	agc	ctc	aac	ggc	acc	aag	gtg	gct	gag	ggc	2091
Thr	Tyr	Tyr	Asp	Leu	Leu	Ser	Leu	Asn	Gly	Thr	Lys	Val	Ala	Glu	Gly	
		640					645					650				
cac	aag	gcc	agc	ttc	tgc	ctg	gag	gac	act	gag	tgt	gag	gga	gac	att	2139
His	Lys	Ala	Ser	Phe	Cys	Leu	Glu	Asp	Thr	Glu	Cys	Glu	Gly	Asp	Ile	
	655					660					665					
cag	aag	agt	tac	gag	tgt	gcc	aac	ttt	gga	gaa	caa	ggc	atc	acc	atg	2187
Gln	Lys	Ser	Tyr	Glu	Cys	Ala	Asn	Phe	Gly	Glu	Gln	Gly	Ile	Thr	Met	
670					675					680					685	
ggc	tgc	tgg	gac	atg	tac	cgt	cat	gac	att	gac	tgc	cag	tgg	ata	gac	2235
Gly	Cys	Trp	Asp	Met	Tyr	Arg	His	Asp	Ile	Asp	Cys	Gln	Trp	Ile	Asp	
			690						695					700		
atc	acc	gat	gtg	ccc	cct	gga	gac	tac	ctg	ttc	cag	gtt	gtc	att	aac	2283
Ile	Thr	Asp	Val	Pro	Pro	Gly	Asp	Tyr	Leu	Phe	Gln	Val	Val	Ile	Asn	
		705						710					715			
ccc	aac	tat	gaa	gtg	cca	gaa	tca	gat	ttc	tct	aac	aac	atc	atg	aag	2331
Pro	Asn	Tyr	Glu	Val	Pro	Glu	Ser	Asp	Phe	Ser	Asn	Asn	Ile	Met	Lys	
		720					725					730				
tgc	agg	agc	cgc	tat	gat	ggc	tac	cgc	atc	tgg	atg	tac	aac	tgt	cac	2379
Cys	Arg	Ser	Arg	Tyr	Asp	Gly	Tyr	Arg	Ile	Trp	Met	Tyr	Asn	Cys	His	
	735					740					745					
gta	ggt	gga	gcc	ttc	agt	gag	gag	aca	gaa	cag	aag	ttc	gaa	cac	ttc	2427
Val	Gly	Gly	Ala	Phe	Ser	Glu	Glu	Thr	Glu	Gln	Lys	Phe	Glu	His	Phe	
750					755					760					765	
agt	gga	ctt	cta	aat	aac	cag	ctc	tct	gta	cag	taa	agaagatcct				2473
Ser	Gly	Leu	Leu	Asn	Asn	Gln	Leu	Ser	Val	Gln						
			770					775								
gggccaggca	tgatggctca	tgccctgtaat	ccctgcactc	atgctgaggc	aggaggattg											2533
ccacaagatt	tccactctgg	acattaaacc	aagcttcagt	ttcaaaagaa	atgaatgaaa											2593
gaaaggaagg	aaggaaggaa	ggaaggaagg	aaggaaggaa	ggaaggaagg	aagaaagggg											2653
aaagggaaaag	ggaagaaaaa	tgacttaatg	gtcacttact	gactcctggg	ggaataactga											2713
ttaccacctc	ttttctagcc	agatccagct	gagaagaaag	gtgctcattc	actccccaga											2773
cactgccgtg	tgtccctgtc	ctgaggcctt	aggggcaggg	ctcgggcaca	tggccatgga											2833
aacttgatga	caagcttaga	gcagcttata	ccatccgagc	tttggcatgt	cccaagtgtg											2893
acatcatctg	tgctctgcac	agaggggccc	ttttcttctg	ggaacacagc	aggcatgaac											2953
tcagcaactg	cagaggtgat	cgggctgaac	tccgtttttc	cccttcttag	gtcatttctg											3013
gaaaacttga	atatcaagac	ctctgtatta	agtttgtttg	gttttttggt	t											3064

<210> 18
<211> 776
<212> PRT
<213> Mouse

<400> 18

Met Glu Leu His Phe Gly Ser Cys Leu Ser Gly Cys Leu Ala Leu Leu
1 5 10 15

Val Leu Leu Pro Ser Leu Ser Leu Ala Gln Tyr Glu Gly Trp Pro Tyr
20 25 30

Gln Leu Gln Tyr Pro Glu Tyr Phe Gln Gln Pro Ala Pro Glu His His
35 40 45

Gln Arg Gln Val Pro Ser Asp Val Val Lys Ile Gln Val Arg Leu Ala
50 55 60

Gly Gln Lys Arg Lys His Asn Glu Gly Arg Val Glu Val Tyr Tyr Glu
65 70 75 80

Gly Gln Trp Gly Thr Val Cys Asp Asp Asp Phe Ser Ile His Ala Ala
85 90 95

His Val Val Cys Arg Gln Val Gly Tyr Val Glu Ala Lys Ser Trp Ala
100 105 110

Ala Ser Ser Ser Tyr Gly Pro Gly Glu Gly Pro Ile Trp Leu Asp Asn
115 120 125

Ile Tyr Cys Thr Gly Lys Glu Ser Thr Leu Ala Ser Cys Ser Ser Asn
130 135 140

Gly Trp Gly Val Thr Asp Cys Lys His Thr Glu Asp Val Gly Val Val
145 150 155 160

Cys Ser Glu Lys Arg Ile Pro Gly Phe Lys Phe Asp Asn Ser Leu Ile
165 170 175

Asn Gln Ile Glu Ser Leu Asn Ile Gln Val Glu Asp Ile Arg Ile Arg
180 185 190

Pro Ile Leu Ser Ala Phe Arg His Arg Lys Pro Val Thr Glu Gly Tyr
195 200 205

Val Glu Val Lys Glu Gly Lys Ala Trp Lys Gln Ile Cys Asn Lys His

210	215	220
Trp Thr Ala Lys Asn Ser His Val Val Cys Gly Met Phe Gly Phe Pro 225 230 235 240		
Ala Glu Lys Thr Tyr Asn Pro Lys Ala Tyr Lys Thr Phe Ala Ser Arg 245 250 255		
Arg Lys Leu Arg Tyr Trp Lys Phe Ser Met Asn Cys Thr Gly Thr Glu 260 265 270		
Ala His Ile Ser Ser Cys Lys Leu Gly Pro Ser Val Thr Arg Asp Pro 275 280 285		
Val Lys Asn Ala Thr Cys Glu Asn Gly Gln Pro Ala Val Val Ser Cys 290 295 300		
Val Pro Ser Gln Ile Phe Ser Pro Asp Gly Pro Ser Arg Phe Arg Lys 305 310 315 320		
Ala Tyr Lys Pro Glu Gln Pro Leu Val Arg Leu Arg Gly Gly Ala Gln 325 330 335		
Val Gly Glu Gly Arg Val Glu Val Leu Lys Asn Gly Glu Trp Gly Thr 340 345 350		
Ile Cys Asp Asp Lys Trp Asp Leu Val Ser Ala Ser Val Val Cys Arg 355 360 365		
Glu Leu Gly Phe Gly Thr Ala Lys Glu Ala Ile Thr Gly Ser Arg Leu 370 375 380		
Gly Gln Gly Ile Gly Pro Ile His Leu Asn Glu Val Gln Cys Thr Gly 385 390 395 400		
Thr Glu Lys Ser Ile Ile Asp Cys Lys Phe Asn Thr Glu Ser Gln Gly 405 410 415		
Cys Asn His Glu Glu Asp Ala Gly Val Arg Cys Asn Ile Pro Ile Met 420 425 430		
Gly Phe Gln Lys Lys Val Arg Leu Asn Gly Gly Arg Asn Pro Tyr Glu 435 440 445		
Gly Arg Val Glu Val Leu Thr Glu Arg Asn Gly Ser Leu Val Trp Gly		

450	455	460
Thr Val Cys Gly Gln Asn Trp Gly Ile Val Glu Ala Met Val Val Cys 465 470 475 480		
Arg Gln Leu Gly Leu Gly Phe Ala Ser Asn Ala Phe Gln Glu Thr Trp 485 490 495		
Tyr Trp His Gly Asn Ile Phe Ala Asn Asn Val Val Met Ser Gly Val 500 505 510		
Lys Cys Ser Gly Thr Glu Leu Ser Leu Ala His Cys Arg His Asp Glu 515 520 525		
Glu Val Ala Cys Pro Glu Gly Gly Val Arg Phe Gly Ala Gly Val Ala 530 535 540		
Cys Ser Glu Thr Ala Pro Asp Leu Val Leu Asn Ala Glu Ile Val Gln 545 550 555 560		
Gln Thr Ala Tyr Leu Glu Asp Arg Pro Met Ser Leu Leu Gln Cys Ala 565 570 575		
Met Glu Glu Asn Cys Leu Ser Ala Ser Ala Val His Thr Asp Pro Thr 580 585 590		
Arg Gly His Arg Arg Leu Leu Arg Phe Ser Ser Gln Ile His Asn Asn 595 600 605		
Gly Gln Ser Asp Phe Arg Pro Lys Asn Gly Arg His Ala Trp Ile Trp 610 615 620		
His Asp Cys His Arg His Tyr His Ser Met Glu Val Phe Thr Tyr Tyr 625 630 635 640		
Asp Leu Leu Ser Leu Asn Gly Thr Lys Val Ala Glu Gly His Lys Ala 645 650 655		
Ser Phe Cys Leu Glu Asp Thr Glu Cys Glu Gly Asp Ile Gln Lys Ser 660 665 670		
Tyr Glu Cys Ala Asn Phe Gly Glu Gln Gly Ile Thr Met Gly Cys Trp 675 680 685		
Asp Met Tyr Arg His Asp Ile Asp Cys Gln Trp Ile Asp Ile Thr Asp		

690	695	700	
Val Pro Pro Gly Asp Tyr Leu Phe Gln Val Val Ile Asn Pro Asn Tyr			
705	710	715	720
Glu Val Pro Glu Ser Asp Phe Ser Asn Asn Ile Met Lys Cys Arg Ser			
	725	730	735
Arg Tyr Asp Gly Tyr Arg Ile Trp Met Tyr Asn Cys His Val Gly Gly			
	740	745	750
Ala Phe Ser Glu Glu Thr Glu Gln Lys Phe Glu His Phe Ser Gly Leu			
	755	760	765
Leu Asn Asn Gln Leu Ser Val Gln			
	770	775	
<210> 19			
<211> 3276			
<212> DNA			
<213> Mouse			
<220>			
<221> CDS			
<222> (148)..(2763)			
<400> 19			
ttgggccagt ggctgtcac tgggttctcc gctcttatgt tggaaagtgt gagggacaca			60
ggagcgacct gcatacctga gcctccgaga gagaagctgc actctggcat ccagtagcag			120
caggagacta agcagataaaa aggagcc atg act tct ggc gct agt cat atg ctg			174
	Met Thr Ser Gly Ala Ser His Met Leu		
	1 5		
gaa gct gcc ctg gag cag atg gac ggg atc att gca ggc act aaa aca			222
Glu Ala Ala Leu Glu Gln Met Asp Gly Ile Ile Ala Gly Thr Lys Thr			
10 15 20 25			
gct gca gat ttt agt gat ggt acc tgt gag cct ggg ctg tct ccc cca			270
Ala Ala Asp Phe Ser Asp Gly Thr Cys Glu Pro Gly Leu Ser Pro Pro			
	30 35 40		
tcc acc tgc ttg aac tcc atg cct gtg ctc cat ctc att gag gac ctg			318
Ser Thr Cys Leu Asn Ser Met Pro Val Leu His Leu Ile Glu Asp Leu			
	45 50 55		
aga cta gcc ttg gag atg ttg gca ctt cct cag gaa aga gaa gcc ctc			366
Arg Leu Ala Leu Glu Met Leu Ala Leu Pro Gln Glu Arg Glu Ala Leu			
	60 65 70		
ctg agc cag gtc cct ggc cca aca gct acc tac ata aag gag tgg ttt			414
Leu Ser Gln Val Pro Gly Pro Thr Ala Thr Tyr Ile Lys Glu Trp Phe			

75	80	85	
gag gac agc ttg tcc Glu Asp Ser Leu Ser 90	cag gta aat cac cac Gln Val Asn His His 95	ggt gct gct agt aat gaa Gly Ala Ala Ser Asn Glu 100	462
acc tac cag gaa cgc ctg gca cgg cta gaa gga gat aaa gag tcc ctc Thr Tyr Gln Glu Arg Leu Ala Arg Leu Glu Gly Asp Lys Glu Ser Leu 110		115	510
ata cta cag gtg agc gtc ctc aca gat caa gtg gaa gcc caa gga gag Ile Leu Gln Val Ser Val Leu Thr Asp Gln Val Glu Ala Gln Gly Glu 125		130	558
aag att cgg gac ctt gaa gtg tgt ctg gaa ggc cac cag gtg aag ctc Lys Ile Arg Asp Leu Glu Val Cys Leu Glu Gly His Gln Val Lys Leu 140		145	606
aat gct gca gaa gag atg ctt cag cag gag ctg cta agt cgc aca tct Asn Ala Ala Glu Glu Met Leu Gln Gln Glu Leu Leu Ser Arg Thr Ser 155		160	654
ctg gag acc cag aag ttg gat ctg atg act gag gtg tct gag ctg aag Leu Glu Thr Gln Lys Leu Asp Leu Met Thr Glu Val Ser Glu Leu Lys 170		175	702
ctc aag ctg gtt ggt atg gaa aaa gaa cag aaa gaa caa gaa gaa aaa Leu Lys Leu Val Gly Met Glu Lys Glu Gln Lys Glu Gln Glu Glu Lys 190		195	750
cag aga aaa gca gag gag tta ctg caa gag ctt aag cac ctc aaa atc Gln Arg Lys Ala Glu Glu Leu Leu Gln Glu Leu Lys His Leu Lys Ile 205		210	798
aag gtg gag gag ctg gag aac gag cgg aac cag tat gag tgg gag ctg Lys Val Glu Glu Leu Glu Asn Glu Arg Asn Gln Tyr Glu Trp Glu Leu 220		225	846
aag gcc acc aag gct gag gta gcc cag ctg caa gaa cag gtg gcc cta Lys Ala Thr Lys Ala Glu Val Ala Gln Leu Gln Glu Gln Val Ala Leu 235		240	894
aaa gat gca gaa att gag cgt ctc cac agc cag ctc tcc cgg agt gca Lys Asp Ala Glu Ile Glu Arg Leu His Ser Gln Leu Ser Arg Ser Ala 250		255	942
gct ctc cac agc gac cat gca gag cga gat caa gaa atc cac cgt ctg Ala Leu His Ser Asp His Ala Glu Arg Asp Gln Glu Ile His Arg Leu 270		275	990
aaa atg ggg atg gaa aca ctg ctg gtt gcc aat gag gat aag gac cgt Lys Met Gly Met Glu Thr Leu Leu Val Ala Asn Glu Asp Lys Asp Arg 285		290	1038
cgg ata gag gag ctg aca ggg ctg ttg aac aag tac cta agg gta aag Arg Ile Glu Glu Leu Thr Gly Leu Leu Asn Lys Tyr Leu Arg Val Lys 300		305	1086
gag att gtg atg gca act cag ggg cct tca gaa aga acc ctc tcc atc Glu Ile Val Met Ala Thr Gln Gly Pro Ser Glu Arg Thr Leu Ser Ile			1134

315	320	325	
aat gaa gat gaa ata gag gga agc ttc cga aaa tgg aat acc aca aat Asn Glu Asp Glu Ile Glu Gly Ser Phe Arg Lys Trp Asn Thr Thr Asn 330 335 340 345			1182
aaa agc cca gag gaa gtc ccg aag caa gag ata tca cca cga tgc agc Lys Ser Pro Glu Glu Val Pro Lys Gln Glu Ile Ser Pro Arg Cys Ser 350 355 360			1230
tct ccc acc cca gga cca cct cct ttg cca cag aaa tca ctg gag agc Ser Pro Thr Pro Gly Pro Pro Pro Leu Pro Gln Lys Ser Leu Glu Ser 365 370 375			1278
agg gct cag aag aaa ctc tcc tgc agt cta gaa gac ttg aga cgt gaa Arg Ala Gln Lys Lys Leu Ser Cys Ser Leu Glu Asp Leu Arg Arg Glu 380 385 390			1326
tct ggg gat aag tgt gtc gat ggg aac cag ctg tcc cca gtg gga gag Ser Gly Asp Lys Cys Val Asp Gly Asn Gln Leu Ser Pro Val Gly Glu 395 400 405			1374
ccc aag gac agc tct ttc cta gcg gag cag aaa tac ccc aca tta cct Pro Lys Asp Ser Ser Phe Leu Ala Glu Gln Lys Tyr Pro Thr Leu Pro 410 415 420 425			1422
ggg aag ctt tca gga gcc aca ccc aat gga gaa gct gcc aaa tct cct Gly Lys Leu Ser Gly Ala Thr Pro Asn Gly Glu Ala Ala Lys Ser Pro 430 435 440			1470
ccc act gcc tcc ctc cag cct gac tct tca ggg agc agc cag cca aag Pro Thr Ala Ser Leu Gln Pro Asp Ser Ser Gly Ser Ser Gln Pro Lys 445 450 455			1518
ctg aga gac aca gaa gga ggc tgg gaa gat ata gtc tca tct gct tcg Leu Arg Asp Thr Glu Gly Gly Trp Glu Asp Ile Val Ser Ser Ala Ser 460 465 470			1566
tct ggg act gag tca agc cct cag tct ccc gtg aca cca gat ggc aaa Ser Gly Thr Glu Ser Ser Pro Gln Ser Pro Val Thr Pro Asp Gly Lys 475 480 485			1614
cgg agc ccc aaa ggc att aag aag ttc tgg gga aag atc cga aga act Arg Ser Pro Lys Gly Ile Lys Lys Phe Trp Gly Lys Ile Arg Arg Thr 490 495 500 505			1662
cag tct gga aac ttc aat act gat gca ccg ggg atg gca gag ttt cga Gln Ser Gly Asn Phe Asn Thr Asp Ala Pro Gly Met Ala Glu Phe Arg 510 515 520			1710
cga ggt ggg ctc cga gca act gcg gga cca agg ctt tct agg acc agg Arg Gly Gly Leu Arg Ala Thr Ala Gly Pro Arg Leu Ser Arg Thr Arg 525 530 535			1758
gac acc aag gga cag aaa tgt gat gcc aat gcc ccc ttt gcc cag tgg Asp Thr Lys Gly Gln Lys Cys Asp Ala Asn Ala Pro Phe Ala Gln Trp 540 545 550			1806
agc aca gaa cgc gta tgt aca tgg atg gag gat ttc ggc ctg ggt cag Ser Thr Glu Arg Val Cys Thr Trp Met Glu Asp Phe Gly Leu Gly Gln			1854

555	560	565	
tat gtg atc ttt gcc aga cag tgg gtg aca tct gga cat aca cta ctg Tyr Val Ile Phe Ala Arg Gln Trp Val Thr Ser Gly His Thr Leu Leu 570 575 580 585			1902
aca gct acc cct cag gac atg gaa aag gag cta ggg att aaa cac ccc Thr Ala Thr Pro Gln Asp Met Glu Lys Glu Leu Gly Ile Lys His Pro 590 595 600			1950
ctc cac agg aag aag ctg gtt tta gca gtg aaa gct atc aac gcc aag Leu His Arg Lys Lys Leu Val Leu Ala Val Lys Ala Ile Asn Ala Lys 605 610 615			1998
caa gaa gaa acg tct gcg ctg ctg gac cac att tgg gtg aca cgg tgg Gln Glu Glu Thr Ser Ala Leu Leu Asp His Ile Trp Val Thr Arg Trp 620 625 630			2046
ctt gat gat att ggc tta ccc caa tac aaa gac cag ttt cat gaa tca Leu Asp Asp Ile Gly Leu Pro Gln Tyr Lys Asp Gln Phe His Glu Ser 635 640 645			2094
aga gtt gat ggg cga atg ctg caa tac cta act gtg aat gat cta ctc Arg Val Asp Gly Arg Met Leu Gln Tyr Leu Thr Val Asn Asp Leu Leu 650 655 660 665			2142
ttc tta aaa gtc acc agc caa cta cat cat ctc agc atc aaa tgt gct Phe Leu Lys Val Thr Ser Gln Leu His His Leu Ser Ile Lys Cys Ala 670 675 680			2190
att cac gtg cta cat gtc aac aag ttc aac ccc aac tgc ctg cac agg Ile His Val Leu His Val Asn Lys Phe Asn Pro Asn Cys Leu His Arg 685 690 695			2238
agg cct gct gat gag agt aac ctt tcc cct tcc gaa gtt gtg cag tgg Arg Pro Ala Asp Glu Ser Asn Leu Ser Pro Ser Glu Val Val Gln Trp 700 705 710			2286
tcc aac cac agg gta atg gag tgg ctg cga tcc gtg gac ctg gca gag Ser Asn His Arg Val Met Glu Trp Leu Arg Ser Val Asp Leu Ala Glu 715 720 725			2334
tat gca ccc aac ctt cga ggg agt ggc gtc cat ggc ggc ctc att atc Tyr Ala Pro Asn Leu Arg Gly Ser Gly Val His Gly Gly Leu Ile Ile 730 735 740 745			2382
ctg gag cct cgc ttt act ggg gac acc ctg gct atg ctt ctt aac atc Leu Glu Pro Arg Phe Thr Gly Asp Thr Leu Ala Met Leu Leu Asn Ile 750 755 760			2430
ccc cca cag aag acg ctc ctc agg cgc cat ctg acc acc aag ttc aac Pro Pro Gln Lys Thr Leu Leu Arg Arg His Leu Thr Thr Lys Phe Asn 765 770 775			2478
gcc ctg att ggt cct gag gct gaa cag gaa aag cga gac aaa atg gcc Ala Leu Ile Gly Pro Glu Ala Glu Gln Glu Lys Arg Asp Lys Met Ala 780 785 790			2526
tca ccc gcc tac aca cct ctg acc acc acc gcc aaa gtt cgg cct agg Ser Pro Ala Tyr Thr Pro Leu Thr Thr Thr Ala Lys Val Arg Pro Arg			2574

795	800	805	
aaa ctt gga ttt tca cat ttt gga aac atg aga aaa aag aag ttt gat			2622
Lys Leu Gly Phe Ser His Phe Gly Asn Met Arg Lys Lys Lys Phe Asp			
810	815	820	825
gaa tct aca gat tac att tgc ccc atg gag cct gga gat gct gtc agt			2670
Glu Ser Thr Asp Tyr Ile Cys Pro Met Glu Pro Gly Asp Ala Val Ser			
	830	835	840
gac agc cac agg gtc tac gga gtc tac cgg ggc ctc agt ccc ctt gac			2718
Asp Ser His Arg Val Tyr Gly Val Tyr Arg Gly Leu Ser Pro Leu Asp			
	845	850	855
aac cat gaa cta gat ggt ttg gac cag gtg gga cag ata agc tga			2763
Asn His Glu Leu Asp Gly Leu Asp Gln Val Gly Gln Ile Ser			
	860	865	870
tgaccctggt atctgccttc tctgtgcacg gagagctcac agtaacactg tgtgtcacca			2823
cgtaactgca cttcaccctc gtccttttgc atgatctaca gaaaacaatt gtgtctttgg			2883
gctgggtctca ctacacactt taaggatggt cagaatatgc agttatacag ccacaaaggg			2943
gacagacttt ggggaactat agccaaatgt ggactctggg aaaacacctg cagacattag			3003
tagatgttta gtaattcata gtatccatgt ttcagcttga aacacatgag cagagggcag			3063
gccctgggta atcgcaaaaag gttcagttct cagacgctgc ccctattctt cagtcgaggg			3123
aagaattcaa gtgccttagg tttgtgagcc acaaagtctt ggctgagatc aaagtgccaa			3183
cagcggatgt ttggaccata gtgacaatgt aatttgattg taccttacta tagagtggcc			3243
acttgtttct gataataaaa acaatattta tgt			3276
<210>	20		
<211>	871		
<212>	PRT		
<213>	Mouse		
<400>	20		
Met Thr Ser Gly Ala Ser His Met Leu Glu Ala Ala Leu Glu Gln Met			
1	5	10	15
Asp Gly Ile Ile Ala Gly Thr Lys Thr Ala Ala Asp Phe Ser Asp Gly			
	20	25	30
Thr Cys Glu Pro Gly Leu Ser Pro Pro Ser Thr Cys Leu Asn Ser Met			
	35	40	45
Pro Val Leu His Leu Ile Glu Asp Leu Arg Leu Ala Leu Glu Met Leu			
	50	55	60

Ala Leu Pro Gln Glu Arg Glu Ala Leu Leu Ser Gln Val Pro Gly Pro
 65 70 75 80

Thr Ala Thr Tyr Ile Lys Glu Trp Phe Glu Asp Ser Leu Ser Gln Val
 85 90 95

Asn His His Gly Ala Ala Ser Asn Glu Thr Tyr Gln Glu Arg Leu Ala
 100 105 110

Arg Leu Glu Gly Asp Lys Glu Ser Leu Ile Leu Gln Val Ser Val Leu
 115 120 125

Thr Asp Gln Val Glu Ala Gln Gly Glu Lys Ile Arg Asp Leu Glu Val
 130 135 140

Cys Leu Glu Gly His Gln Val Lys Leu Asn Ala Ala Glu Glu Met Leu
 145 150 155 160

Gln Gln Glu Leu Leu Ser Arg Thr Ser Leu Glu Thr Gln Lys Leu Asp
 165 170 175

Leu Met Thr Glu Val Ser Glu Leu Lys Leu Lys Leu Val Gly Met Glu
 180 185 190

Lys Glu Gln Lys Glu Gln Glu Glu Lys Gln Arg Lys Ala Glu Glu Leu
 195 200 205

Leu Gln Glu Leu Lys His Leu Lys Ile Lys Val Glu Glu Leu Glu Asn
 210 215 220

Glu Arg Asn Gln Tyr Glu Trp Glu Leu Lys Ala Thr Lys Ala Glu Val
 225 230 235 240

Ala Gln Leu Gln Glu Gln Val Ala Leu Lys Asp Ala Glu Ile Glu Arg
 245 250 255

Leu His Ser Gln Leu Ser Arg Ser Ala Ala Leu His Ser Asp His Ala
 260 265 270

Glu Arg Asp Gln Glu Ile His Arg Leu Lys Met Gly Met Glu Thr Leu
 275 280 285

Leu Val Ala Asn Glu Asp Lys Asp Arg Arg Ile Glu Glu Leu Thr Gly
 290 295 300

Leu Leu Asn Lys Tyr Leu Arg Val Lys Glu Ile Val Met Ala Thr Gln
 305 310 315 320
 Gly Pro Ser Glu Arg Thr Leu Ser Ile Asn Glu Asp Glu Ile Glu Gly
 325 330 335
 Ser Phe Arg Lys Trp Asn Thr Thr Asn Lys Ser Pro Glu Glu Val Pro
 340 345 350
 Lys Gln Glu Ile Ser Pro Arg Cys Ser Ser Pro Thr Pro Gly Pro Pro
 355 360 365
 Pro Leu Pro Gln Lys Ser Leu Glu Ser Arg Ala Gln Lys Lys Leu Ser
 370 375 380
 Cys Ser Leu Glu Asp Leu Arg Arg Glu Ser Gly Asp Lys Cys Val Asp
 385 390 395 400
 Gly Asn Gln Leu Ser Pro Val Gly Glu Pro Lys Asp Ser Ser Phe Leu
 405 410 415
 Ala Glu Gln Lys Tyr Pro Thr Leu Pro Gly Lys Leu Ser Gly Ala Thr
 420 425 430
 Pro Asn Gly Glu Ala Ala Lys Ser Pro Pro Thr Ala Ser Leu Gln Pro
 435 440 445
 Asp Ser Ser Gly Ser Ser Gln Pro Lys Leu Arg Asp Thr Glu Gly Gly
 450 455 460
 Trp Glu Asp Ile Val Ser Ser Ala Ser Ser Gly Thr Glu Ser Ser Pro
 465 470 475 480
 Gln Ser Pro Val Thr Pro Asp Gly Lys Arg Ser Pro Lys Gly Ile Lys
 485 490 495
 Lys Phe Trp Gly Lys Ile Arg Arg Thr Gln Ser Gly Asn Phe Asn Thr
 500 505 510
 Asp Ala Pro Gly Met Ala Glu Phe Arg Arg Gly Gly Leu Arg Ala Thr
 515 520 525
 Ala Gly Pro Arg Leu Ser Arg Thr Arg Asp Thr Lys Gly Gln Lys Cys
 530 535 540

Asp Ala Asn Ala Pro Phe Ala Gln Trp Ser Thr Glu Arg Val Cys Thr
 545 550 555 560

Trp Met Glu Asp Phe Gly Leu Gly Gln Tyr Val Ile Phe Ala Arg Gln
 565 570 575

Trp Val Thr Ser Gly His Thr Leu Leu Thr Ala Thr Pro Gln Asp Met
 580 585 590

Glu Lys Glu Leu Gly Ile Lys His Pro Leu His Arg Lys Lys Leu Val
 595 600 605

Leu Ala Val Lys Ala Ile Asn Ala Lys Gln Glu Glu Thr Ser Ala Leu
 610 615 620

Leu Asp His Ile Trp Val Thr Arg Trp Leu Asp Asp Ile Gly Leu Pro
 625 630 635 640

Gln Tyr Lys Asp Gln Phe His Glu Ser Arg Val Asp Gly Arg Met Leu
 645 650 655

Gln Tyr Leu Thr Val Asn Asp Leu Leu Phe Leu Lys Val Thr Ser Gln
 660 665 670

Leu His His Leu Ser Ile Lys Cys Ala Ile His Val Leu His Val Asn
 675 680 685

Lys Phe Asn Pro Asn Cys Leu His Arg Arg Pro Ala Asp Glu Ser Asn
 690 695 700

Leu Ser Pro Ser Glu Val Val Gln Trp Ser Asn His Arg Val Met Glu
 705 710 715 720

Trp Leu Arg Ser Val Asp Leu Ala Glu Tyr Ala Pro Asn Leu Arg Gly
 725 730 735

Ser Gly Val His Gly Gly Leu Ile Ile Leu Glu Pro Arg Phe Thr Gly
 740 745 750

Asp Thr Leu Ala Met Leu Leu Asn Ile Pro Pro Gln Lys Thr Leu Leu
 755 760 765

Arg Arg His Leu Thr Thr Lys Phe Asn Ala Leu Ile Gly Pro Glu Ala
 770 775 780

Glu Gln Glu Lys Arg Asp Lys Met Ala Ser Pro Ala Tyr Thr Pro Leu
785 790 795 800

Thr Thr Thr Ala Lys Val Arg Pro Arg Lys Leu Gly Phe Ser His Phe
805 810 815

Gly Asn Met Arg Lys Lys Lys Phe Asp Glu Ser Thr Asp Tyr Ile Cys
820 825 830

Pro Met Glu Pro Gly Asp Ala Val Ser Asp Ser His Arg Val Tyr Gly
835 840 845

Val Tyr Arg Gly Leu Ser Pro Leu Asp Asn His Glu Leu Asp Gly Leu
850 855 860

Asp Gln Val Gly Gln Ile Ser
865 870

<210> 21
<211> 5020
<212> DNA
<213> Mouse

<220>
<221> CDS
<222> (174)..(1277)

<400> 21
tgcaggggcta gtctgtttggc ctgacgtcag atgtcgcttt gacaaacgcc cccgggggct 60
gaggaaggct ctccgctgct ctgatggggc agcccagtcg tggcccagct ccctggagag 120
gcatccgcat cctctgggct gagccgtagc tcctgtgacg ctgacttcca ggc atg 176
Met
1
agg tgg ctc ctg ccc tgg acg ctg gca gcc gtg gca gtc ctg agg gtg 224
Arg Trp Leu Leu Pro Trp Thr Leu Ala Ala Val Ala Val Leu Arg Val
5 10 15
ggc aac atc ctg gcc acg gcc ctc tct cca acc ccc aca aca atg acc 272
Gly Asn Ile Leu Ala Thr Ala Leu Ser Pro Thr Pro Thr Thr Met Thr
20 25 30
ttc acc cca gca cca cta gag gaa acg act aca cgc ccc gaa ttc tgc 320
Phe Thr Pro Ala Pro Leu Glu Glu Thr Thr Thr Arg Pro Glu Phe Cys
35 40 45
aag tgg cca tgt gag tgc cca caa tcc cca cct cgc tgc cca ctg ggc 368
Lys Trp Pro Cys Glu Cys Pro Gln Ser Pro Pro Arg Cys Pro Leu Gly
50 55 60 65
gtc agc cta atc aca gat ggc tgt gaa tgc tgt aag ata tgt gcc cag 416

Val	Ser	Leu	Ile	Thr	Asp	Gly	Cys	Glu	Cys	Cys	Lys	Ile	Cys	Ala	Gln	
				70					75					80		
cag	ctt	ggg	gac	aac	tgc	aca	gag	gct	gcc	atc	tgt	gac	cca	cac	cgg	464
Gln	Leu	Gly	Asp	Asn	Cys	Thr	Glu	Ala	Ala	Ile	Cys	Asp	Pro	His	Arg	
			85					90					95			
ggc	ctc	tac	tgc	gat	tac	agt	ggg	gat	cgc	ccg	agg	tac	gca	ata	gga	512
Gly	Leu	Tyr	Cys	Asp	Tyr	Ser	Gly	Asp	Arg	Pro	Arg	Tyr	Ala	Ile	Gly	
		100					105					110				
gtg	tgt	gca	cag	gtg	gtc	ggg	gtg	ggc	tgt	gtc	ctg	gat	ggc	gta	cgc	560
Val	Cys	Ala	Gln	Val	Val	Gly	Val	Gly	Cys	Val	Leu	Asp	Gly	Val	Arg	
	115					120					125					
tac	acc	aac	ggc	gag	tcc	ttc	caa	ccc	aac	tgc	agg	tac	aac	tgt	acc	608
Tyr	Thr	Asn	Gly	Glu	Ser	Phe	Gln	Pro	Asn	Cys	Arg	Tyr	Asn	Cys	Thr	
130					135				140						145	
tgc	att	gat	ggc	acg	gtg	ggc	tgc	aca	ccg	ctg	tgc	cta	agc	ccc	agg	656
Cys	Ile	Asp	Gly	Thr	Val	Gly	Cys	Thr	Pro	Leu	Cys	Leu	Ser	Pro	Arg	
				150					155					160		
ccc	cca	cgc	ctc	tgg	tgc	cgc	cag	ccc	cgg	cac	gtg	aga	gtc	cct	ggc	704
Pro	Pro	Arg	Leu	Trp	Cys	Arg	Gln	Pro	Arg	His	Val	Arg	Val	Pro	Gly	
			165					170					175			
cag	tgc	tgt	gag	cag	tgg	gtg	tgt	gat	gat	gac	gca	agg	aga	cca	cgc	752
Gln	Cys	Cys	Glu	Gln	Trp	Val	Cys	Asp	Asp	Asp	Ala	Arg	Arg	Pro	Arg	
		180					185					190				
cag	act	gca	ctg	ttg	gac	acc	aga	gcc	ttt	gca	gcg	tca	ggc	gcc	gtg	800
Gln	Thr	Ala	Leu	Leu	Asp	Thr	Arg	Ala	Phe	Ala	Ala	Ser	Gly	Ala	Val	
	195					200					205					
gag	caa	cgg	tat	gag	aac	tgc	ata	gcc	tac	act	agt	ccc	tgg	agc	ccc	848
Glu	Gln	Arg	Tyr	Glu	Asn	Cys	Ile	Ala	Tyr	Thr	Ser	Pro	Trp	Ser	Pro	
210					215					220					225	
tgc	tct	acc	acc	tgt	ggc	cta	ggg	atc	tcc	act	cgg	atc	tct	aac	gtc	896
Cys	Ser	Thr	Thr	Cys	Gly	Leu	Gly	Ile	Ser	Thr	Arg	Ile	Ser	Asn	Val	
				230					235					240		
aac	gcc	cgg	tgc	tgg	cca	gag	cag	gaa	agt	cgc	ctc	tgc	aac	ctg	cgg	944
Asn	Ala	Arg	Cys	Trp	Pro	Glu	Gln	Glu	Ser	Arg	Leu	Cys	Asn	Leu	Arg	
			245					250					255			
cca	tgt	gat	gtg	gac	atc	caa	cta	cac	atc	aag	gca	ggg	aag	aaa	tgc	992
Pro	Cys	Asp	Val	Asp	Ile	Gln	Leu	His	Ile	Lys	Ala	Gly	Lys	Lys	Cys	
		260					265					270				
ctg	gct	gtg	tac	cag	cca	gag	gag	gcc	acg	aac	ttc	act	ctc	gca	ggc	1040
Leu	Ala	Val	Tyr	Gln	Pro	Glu	Glu	Ala	Thr	Asn	Phe	Thr	Leu	Ala	Gly	
	275					280					285					
tgt	gtc	agc	aca	cgc	acc	tac	cga	ccc	aag	tac	tgc	gga	gtc	tgt	act	1088
Cys	Val	Ser	Thr	Arg	Thr	Tyr	Arg	Pro	Lys	Tyr	Cys	Gly	Val	Cys	Thr	
290					295				300						305	
gac	aac	agg	tgt	tgc	atc	ccc	tac	aag	tcc	aag	acc	atc	agt	gtg	gat	1136

Asp	Asn	Arg	Cys	Cys	Ile	Pro	Tyr	Lys	Ser	Lys	Thr	Ile	Ser	Val	Asp	
				310					315					320		
ttc	cag	tgt	cca	gag	ggg	cca	ggg	ttc	tcc	cgg	cag	gtc	cta	tgg	att	1184
Phe	Gln	Cys	Pro	Glu	Gly	Pro	Gly	Phe	Ser	Arg	Gln	Val	Leu	Trp	Ile	
			325					330					335			
aat	gct	tgc	ttc	tgc	aac	ctg	agc	tgc	agg	aat	cct	aac	gat	atc	ttt	1232
Asn	Ala	Cys	Phe	Cys	Asn	Leu	Ser	Cys	Arg	Asn	Pro	Asn	Asp	Ile	Phe	
		340					345					350				
gct	gac	ttg	gaa	tct	tac	cct	gac	ttc	gaa	gag	att	gcc	aat	tag		1277
Ala	Asp	Leu	Glu	Ser	Tyr	Pro	Asp	Phe	Glu	Glu	Ile	Ala	Asn			
	355					360					365					
gtgggtgtgt	ggctcagggt	aaagtccat	gctgcaaagc	agccagccct	ttgtgggtcca											1337
ggacttcaca	attgagcctt	atttcattcta	cttcctactc	gattctgaat	tcccagtttc											1397
tgttcctggt	ttgacaatcg	taatggccca	ggagagtgt	gctcaggctc	agacaatggg											1457
ttcctccttg	gggacattct	acatcattcc	aaggaaaaca	catctctgac	tgttcacaat											1517
ggaagcaaag	cctggcccag	ctagtctggc	tccagcctgg	gcaagttgtc	agaagttgtg											1577
atgggattgt	ccaagggaaa	gcatcagctg	aagaaccagt	atcatgaagt	ccttcctcag											1637
atgccaagcc	tagggatgct	gggatccttt	cagacagatg	gatgggattg	gggacacagg											1697
aataagctat	tattttaccc	ttgccaaatg	atactatcct	gggtattttct	gcctaaaaca											1757
tacaaaaagt	gttcttggtc	cactgatctg	tatatcacia	gtcaccaaac	attttccagg											1817
tgaggaccat	agtttgtgtc	ttctgttttg	ctattgaaaa	tcattttaaa	aagaaggaaa											1877
aaaaaaaaaa	gaaaagaaaa	gaaagtcatt	tcattaactt	gggcactttc	tcctctcacc											1937
ccatattcta	taaagggtta	aacttgggtt	cttggtgatc	aggaatgtaa	tttgagaagt											1997
cttacttttg	cagggagatg	gtagccctca	attcatcccg	tagatgggac	aaggccagcc											2057
aatctttcaa	gccatagctg	ggcaggtcac	tgaatctgct	gctggccaag	ttcttaggac											2117
aattagccaa	aatctggggc	tctctctccc	tagggttcat	gggagtttgt	agggaccgta											2177
gagtgacttg	tctgttgtct	caaaaagtaa	gatggaaaga	tgttctcatg	gcccttagaa											2237
gactcttttg	aagtctacgc	cagacctaac	agaatatgtg	catcaaacia	acaagtggat											2297
caccctccca	tggcctgggt	gacctctagc	agtcaccag	tgactgtggg	aaggccacag											2357
tagtccctgg	accaggaca	aatctttttt	gtttcagtga	cctactttac	agcctcagt											2417
tctatgaaga	aagttaactc	agttttctca	tctgaagaca	gaagtcgacc	agccattcag											2477
aaatggggat	ctatttagta	gtggtaaacg	ttaaagagtt	tgtaagctaa	agaaatattt											2537
tttttcctaa	gtgataatga	ggttgttacc	tatttttagag	gtagaatttt	ctgtcatcat											2597
ccttttattg	tgttctacat	actaccatt	gttctcaata	tttgccacac	atttactcat											2657

tgaaacttgc	tgataacaca	gaggacttcc	cttaatgatt	tctgttcttg	acactgtgaa	2717
atatcaattc	aaagaggcta	ataagttcaa	tcaaagtcac	ctatctgaag	actcatagcc	2777
agagaagatt	gccttcatat	ttcccccttg	cttctggacc	ttgtaaacat	gtcagggcag	2837
gaaagcatac	agaagtcagc	agcttgcctt	cttagtattg	gctctctagc	ccctttcacg	2897
taagaggaga	gtgtgtctag	gtactaagga	tccaacctaa	actggacaga	aaagggcatg	2957
tgcattatcc	cctgtggctc	ctcctgcctt	ggaatcagaa	ctagcttaca	gcatgctttt	3017
atatgatgat	tcagtttgcc	ccacaccata	catatgggca	tatgggagaa	ctatacacac	3077
actcataaat	ggatttgtaa	gtaggaaagg	ggacttgaga	tttccccctc	ttcctgcaac	3137
ttcccaaagg	cctggcctta	tgcaaggcaa	acagtgggtgc	ttaagatgta	ttttgggaag	3197
aaaatactat	atatatatat	tcctatTTTT	ccttagaagc	cttttcttcc	aggatctcat	3257
cttaacagta	agaaatcctc	tcttaagaga	ggcctagtat	tttgagtaaa	catatgttca	3317
tatgtgtaca	agtacttgta	tgtaaataata	agttaccact	gtgggttatt	aattaggtaa	3377
atTTtatgtg	gtatcatatt	tgattttctt	ctattggaaa	aatctgcctt	aacagctaac	3437
tctgtaagaa	cttccatagg	agccataagc	tagggctctc	ccaggatatcc	atcctctttt	3497
gggaaactga	gctgagcatc	ttcaacccaa	ggagttaggg	tgatcattgg	gaataggaga	3557
aagggatggc	cagggtagct	ccatcgttat	ttagaaacag	acctggcata	cagaacgacc	3617
agaggaacca	accttctttg	aaccaaggga	aaaagacttg	gatgtaatat	atagaagctt	3677
tttctaatag	tcagaaacag	actttaattg	tatggcctgg	ttcaaggaaa	gttaagaatg	3737
tccattatcg	ttaaaaacaa	aagtccatta	ttgatagctt	atTTggtgct	aagccctacg	3797
gtgcattttg	tccggctatc	acttagcaga	gccatgctca	gtacacagtc	tttctctatt	3857
caataaatag	aaacgctgaa	gctcaaaggc	actgaggagc	tgaggctcag	aagcatgttt	3917
agtccactct	atcagggggg	gaagagatct	tgacggaacc	taaatgacta	ctattggaaa	3977
ctcatatTTg	aaagctttca	gaagtcccac	ccccacccca	tccccagatg	cttagaaact	4037
aaagaagcaa	tgaggatgag	ctagccttca	gtgaagaggt	tcactactgc	accaagagtg	4097
aatgtcttag	gtgtacttag	tcattggaca	gggagacctg	agtgagtttg	tgaacctgca	4157
gcttactaaa	ccttacaatg	agcatttgga	gagccaagac	tgcttctcgg	cgctttactg	4217
acatggcttg	cttaatcttc	tcagtgagcc	caagagtcag	ggcgttacca	ctgcccattt	4277
tagggctgag	aaagcaaaat	ctccaggagt	taagtgattt	gctcaagttt	ttaaccaacc	4337
gaggcactgc	agataaaactc	cgaagccag	tgtcatgtaa	catgccccatg	ccatctctcc	4397
ggacacgcag	cccatttttcc	tgttcctaaa	ccaaaggctc	agagtcacca	gaaccaactc	4457

acaggacagt gcagaaattc taatgtcgag ggtgattaga gactgatcaa agaaagtaat 4517
 ttcaaatgat atgattgttt gtaagcacc tagttaattc tggactacat atgcatagag 4577
 attgtgaaga acattacagc ctgtgactat aacgttgact tctgtcattt ctttttaaag 4637
 acttggtttt tttttttact caaaggaccc acagtgcag ccctgaatgg ttgagaagca 4697
 ttgattagct gtgagtcctg catatgtatg tatgtgtgtg tgtgtgtgtg tatttgtatg 4757
 tacttatcta ttttcaaact gtgattgtgt atttaaatat tcctcctgcc attttgaag 4817
 tgattacgca taaagaaaca cctttgaatg tcctaataaa ggagagctag cccttgggcg 4877
 gcctgtcaca ttttgccaca ttctcattt ttctcatgat ctgtgtagca gggaatgtgt 4937
 ttgttcaacc atgatgagtt ttcattgttc aaattctttg tttacagctt ttctccttaa 4997
 agcaataaat catcagcaac agt 5020

<210> 22
 <211> 367
 <212> PRT
 <213> Mouse

<400> 22

Met Arg Trp Leu Leu Pro Trp Thr Leu Ala Ala Val Ala Val Leu Arg
 1 5 10 15

Val Gly Asn Ile Leu Ala Thr Ala Leu Ser Pro Thr Pro Thr Thr Met
 20 25 30

Thr Phe Thr Pro Ala Pro Leu Glu Glu Thr Thr Thr Arg Pro Glu Phe
 35 40 45

Cys Lys Trp Pro Cys Glu Cys Pro Gln Ser Pro Pro Arg Cys Pro Leu
 50 55 60

Gly Val Ser Leu Ile Thr Asp Gly Cys Glu Cys Cys Lys Ile Cys Ala
 65 70 75 80

Gln Gln Leu Gly Asp Asn Cys Thr Glu Ala Ala Ile Cys Asp Pro His
 85 90 95

Arg Gly Leu Tyr Cys Asp Tyr Ser Gly Asp Arg Pro Arg Tyr Ala Ile
 100 105 110

Gly Val Cys Ala Gln Val Val Gly Val Gly Cys Val Leu Asp Gly Val
 115 120 125

Arg Tyr Thr Asn Gly Glu Ser Phe Gln Pro Asn Cys Arg Tyr Asn Cys
 130 135 140

Thr Cys Ile Asp Gly Thr Val Gly Cys Thr Pro Leu Cys Leu Ser Pro
 145 150 155 160

Arg Pro Pro Arg Leu Trp Cys Arg Gln Pro Arg His Val Arg Val Pro
 165 170 175

Gly Gln Cys Cys Glu Gln Trp Val Cys Asp Asp Asp Ala Arg Arg Pro
 180 185 190

Arg Gln Thr Ala Leu Leu Asp Thr Arg Ala Phe Ala Ala Ser Gly Ala
 195 200 205

Val Glu Gln Arg Tyr Glu Asn Cys Ile Ala Tyr Thr Ser Pro Trp Ser
 210 215 220

Pro Cys Ser Thr Thr Cys Gly Leu Gly Ile Ser Thr Arg Ile Ser Asn
 225 230 235 240

Val Asn Ala Arg Cys Trp Pro Glu Gln Glu Ser Arg Leu Cys Asn Leu
 245 250 255

Arg Pro Cys Asp Val Asp Ile Gln Leu His Ile Lys Ala Gly Lys Lys
 260 265 270

Cys Leu Ala Val Tyr Gln Pro Glu Glu Ala Thr Asn Phe Thr Leu Ala
 275 280 285

Gly Cys Val Ser Thr Arg Thr Tyr Arg Pro Lys Tyr Cys Gly Val Cys
 290 295 300

Thr Asp Asn Arg Cys Cys Ile Pro Tyr Lys Ser Lys Thr Ile Ser Val
 305 310 315 320

Asp Phe Gln Cys Pro Glu Gly Pro Gly Phe Ser Arg Gln Val Leu Trp
 325 330 335

Ile Asn Ala Cys Phe Cys Asn Leu Ser Cys Arg Asn Pro Asn Asp Ile
 340 345 350

Phe Ala Asp Leu Glu Ser Tyr Pro Asp Phe Glu Glu Ile Ala Asn
 355 360 365

<210> 23
 <211> 1580
 <212> DNA
 <213> Mouse

<220>
 <221> CDS
 <222> (318) .. (794)

<400> 23
 ctgagaagga aaccgcatct tcagacttct gctcactcac gagaggagct aggggtcatcg 60
 gaccctaag atcctttcac atcgctccga ctgcgccgaa cactcctcac cagtttcctc 120
 agccacagcc ctacctgtga gctccggact tccccggctt tctgtggatg ctcaggcaga 180
 ctgcagagac ctagcctagg acagcagtga gggggacact cctctcctct cctctcctct 240
 ggtatcagcg tctcccccaa gggggacgag catggtgatt gtgccttgaa ggaccttggc 300
 tctggatgtc tgagaag atg ctg gtc atg aag ctg ttc act tgc ttc tta 350
 Met Leu Val Met Lys Leu Phe Thr Cys Phe Leu
 1 5 10
 cag gtc cta gct ggg ttg gct gtg cat tcc cag ggg gcc ctg tct gct 398
 Gln Val Leu Ala Gly Leu Ala Val His Ser Gln Gly Ala Leu Ser Ala
 15 20 25
 ggg aac aac tca aca gaa gtg gaa gtg gtg cct ttc aac gaa gtg tgg 446
 Gly Asn Asn Ser Thr Glu Val Glu Val Val Pro Phe Asn Glu Val Trp
 30 35 40
 ggt cgc agc tac tgt cgg ccc atg gag aag ctg gtg tac atc ttg gat 494
 Gly Arg Ser Tyr Cys Arg Pro Met Glu Lys Leu Val Tyr Ile Leu Asp
 45 50 55
 gaa tac cct gat gag gtg tct cac ata ttc agt ccg tcc tgt gtc ctt 542
 Glu Tyr Pro Asp Glu Val Ser His Ile Phe Ser Pro Ser Cys Val Leu
 60 65 70 75
 ctg agt cgc tgt agt ggc tgc tgt ggt gat gaa ggt ctg cac tgt gtg 590
 Leu Ser Arg Cys Ser Gly Cys Cys Gly Asp Glu Gly Leu His Cys Val
 80 85 90
 ccg ata aag aca gcc aac atc act atg cag atc ttg aag att ccc ccc 638
 Pro Ile Lys Thr Ala Asn Ile Thr Met Gln Ile Leu Lys Ile Pro Pro
 95 100 105
 aat cgg gat cca cat ttc tat gtg gag atg aca ttt tct cag gat gtg 686
 Asn Arg Asp Pro His Phe Tyr Val Glu Met Thr Phe Ser Gln Asp Val
 110 115 120
 ctc tgt gaa tgc aga cct att ctg gag acg aca aag gca gaa agg agg 734
 Leu Cys Glu Cys Arg Pro Ile Leu Glu Thr Thr Lys Ala Glu Arg Arg
 125 130 135
 aaa acc aag ggg aag agg aag agg agt aga aac tca cag act gag gaa 782
 Lys Thr Lys Gly Lys Arg Lys Arg Ser Arg Asn Ser Gln Thr Glu Glu

140	145	150	155	
ccc cac ccg tga tgtcatttcc cggaggtaac cagccactca gaggagagcc				834
Pro His Pro				

ccacacccag ctcacgtatt tattaccgtc accctctcag aaccctccct gctggtacct	894
accctctatt tattagccga ctcgctccctg ctgaatgacg tgccccctcc aagataaggg	954
gcatggaagg acaagacgct caggaattca gtgccttaaa acagaacgag agagaaagaa	1014
agaagccagc cacggatctg tgggagcttc ggcttgggaa gaagcaagac atggacatgg	1074
ccttacaagg ggcaagccgc accccagagg ccctggctct ccagggaact ggagaagaga	1134
agaggaggcc tagaacctgc cctgattccc agctccaccc agagagcagc tctggccccg	1194
gctgcattga aggcattgtag aggggaccca gtctactgta tcctggagat gggacaggac	1254
attcggctct ggagagcaga gcttgctgt ggagtttgcc cttcagccta gaagtttatg	1314
cttcaccctt tgcaaaggtc ctttgtcccc tctctggaac acaggcagag tggcctgggg	1374
ctgagcagag ggaggctgg aggagcagta gcccgtggac tttgaccgat acaagtctgg	1434
gttgtgtgtc ttcgtggtac agctacggga agtgagccga ctcttgagg gcccttgag	1494
cccaccggtt gtctctgccc ggactaactg ccaagccaga ttctcttgaa taaagcattc	1554
tagtctggaa aaaaaaaaaa aaaaaa	1580

<210> 24
 <211> 158
 <212> PRT
 <213> Mouse

<400> 24

Met	Leu	Val	Met	Lys	Leu	Phe	Thr	Cys	Phe	Leu	Gln	Val	Leu	Ala	Gly
1				5					10					15	

Leu	Ala	Val	His	Ser	Gln	Gly	Ala	Leu	Ser	Ala	Gly	Asn	Asn	Ser	Thr
			20					25					30		

Glu	Val	Glu	Val	Val	Pro	Phe	Asn	Glu	Val	Trp	Gly	Arg	Ser	Tyr	Cys
	35						40					45			

Arg	Pro	Met	Glu	Lys	Leu	Val	Tyr	Ile	Leu	Asp	Glu	Tyr	Pro	Asp	Glu
	50					55					60				

Val	Ser	His	Ile	Phe	Ser	Pro	Ser	Cys	Val	Leu	Leu	Ser	Arg	Cys	Ser
65					70					75				80	

Gly Cys Cys Gly Asp Glu Gly Leu His Cys Val Pro Ile Lys Thr Ala
85 90 95

Asn Ile Thr Met Gln Ile Leu Lys Ile Pro Pro Asn Arg Asp Pro His
100 105 110

Phe Tyr Val Glu Met Thr Phe Ser Gln Asp Val Leu Cys Glu Cys Arg
115 120 125

Pro Ile Leu Glu Thr Thr Lys Ala Glu Arg Arg Lys Thr Lys Gly Lys
130 135 140

Arg Lys Arg Ser Arg Asn Ser Gln Thr Glu Glu Pro His Pro
145 150 155

<210> 25
<211> 2879
<212> DNA
<213> Mouse

<220>
<221> CDS
<222> (223) .. (2124)

<400> 25
ggcacgaggg ccacccgagt cgccggcggtc gccacctgca cttggctctg gacccccgcg 60
gacagagccc cggccggccg ccgcttcccg ccgcctgccc tgcccacctg ccaggtatta 120
ccacttaaag aaaccctttt accggcaaac ctatgctaaa gagtataagt aacaaaggaa 180
accaaacagt tatctgtcaa gtaacaagca tttaatgaca ga atg gct cac ctt 234
Met Ala His Leu
1
aag cga cta gta aaa ttg cac att aaa aga cat tac cac aga aag ttc 282
Lys Arg Leu Val Lys Leu His Ile Lys Arg His Tyr His Arg Lys Phe
5 10 15 20
tgg aag ctg ggt gca gtc atc ttt ttc ttt tta gta gtt ctg att tta 330
Trp Lys Leu Gly Ala Val Ile Phe Phe Phe Leu Val Val Leu Ile Leu
25 30 35
atg caa aga gaa gta agt gtt cag tat tcc aag gag gaa tca aag atg 378
Met Gln Arg Glu Val Ser Val Gln Tyr Ser Lys Glu Glu Ser Lys Met
40 45 50
gag agg aac ttg aaa aac aaa aac aaa atg ttg gat ttt atg ctc gaa 426
Glu Arg Asn Leu Lys Asn Lys Asn Lys Met Leu Asp Phe Met Leu Glu
55 60 65
gct gta aat aat att aaa gat gca atg cca aag atg caa ata gga gcg 474
Ala Val Asn Asn Ile Lys Asp Ala Met Pro Lys Met Gln Ile Gly Ala
70 75 80

ccc att aag gag aat atc gac gtc cgc gag aga ccc tgt ctg caa ggg	522
Pro Ile Lys Glu Asn Ile Asp Val Arg Glu Arg Pro Cys Leu Gln Gly	
85 90 95 100	
tac tac aca gcc gcg gag ttg aag ccg gtt ttt gat cgc cca cct cag	570
Tyr Tyr Thr Ala Ala Glu Leu Lys Pro Val Phe Asp Arg Pro Pro Gln	
105 110 115	
gat tct aac gca cct ggt gct tct ggc aag ccg ttt aag atc acc cac	618
Asp Ser Asn Ala Pro Gly Ala Ser Gly Lys Pro Phe Lys Ile Thr His	
120 125 130	
ctc agc ccg gag gag cag aag gag aaa gag cga ggg gaa acg aag cac	666
Leu Ser Pro Glu Glu Gln Lys Glu Lys Glu Arg Gly Glu Thr Lys His	
135 140 145	
tgc ttc aac gcc ttt gca agt gac aga att tct ctg cac cgg gac ctt	714
Cys Phe Asn Ala Phe Ala Ser Asp Arg Ile Ser Leu His Arg Asp Leu	
150 155 160	
ggg cct gac acc cga cca cct gaa tgt att gaa caa aaa ttt aag cgc	762
Gly Pro Asp Thr Arg Pro Pro Glu Cys Ile Glu Gln Lys Phe Lys Arg	
165 170 175 180	
tgc ccg ccc ctg cct acc acc agt gtc ata ata gtc ttt cac aat gaa	810
Cys Pro Pro Leu Pro Thr Thr Ser Val Ile Ile Val Phe His Asn Glu	
185 190 195	
gca tgg tcc acg ctg ctt agg acc gtc cac agt gtg ctc tat tct tca	858
Ala Trp Ser Thr Leu Leu Arg Thr Val His Ser Val Leu Tyr Ser Ser	
200 205 210	
cct gcc ata ctg ctg aag gag atc att ttg gtg gat gat gct agt gta	906
Pro Ala Ile Leu Leu Lys Glu Ile Ile Leu Val Asp Asp Ala Ser Val	
215 220 225	
gac gac tac ctg cat gaa aag ctg gag gaa tac ata aaa cag ttt tct	954
Asp Asp Tyr Leu His Glu Lys Leu Glu Glu Tyr Ile Lys Gln Phe Ser	
230 235 240	
att gtg aaa ata gtc agg cag caa gaa agg aaa ggc ctg atc acc gcg	1002
Ile Val Lys Ile Val Arg Gln Gln Glu Arg Lys Gly Leu Ile Thr Ala	
245 250 255 260	
cgg ttg cta ggg gca gct gta gca act gcc gag acg ctc acg ttc tta	1050
Arg Leu Leu Gly Ala Ala Val Ala Thr Ala Glu Thr Leu Thr Phe Leu	
265 270 275	
gat gct cac tgt gag tgc ttc tat ggc tgg ctg gaa cct ctg ctg gcc	1098
Asp Ala His Cys Glu Cys Phe Tyr Gly Trp Leu Glu Pro Leu Leu Ala	
280 285 290	
agg ata gct gag aac tac act gcc gtg gtg agt cca gac atc gca tcc	1146
Arg Ile Ala Glu Asn Tyr Thr Ala Val Val Ser Pro Asp Ile Ala Ser	
295 300 305	
ata gat cta aac aca ttt gaa ttc aac aag cct tct ccg tac gga agc	1194
Ile Asp Leu Asn Thr Phe Glu Phe Asn Lys Pro Ser Pro Tyr Gly Ser	
310 315 320	

aac cat aac cgt gga aat ttt gac tgg agc ctt tcc ttt ggc tgg gag	1242
Asn His Asn Arg Gly Asn Phe Asp Trp Ser Leu Ser Phe Gly Trp Glu	
325 330 335 340	
tca ctt cct gat cat gag aag caa aga agg aaa gat gaa acc tac cca	1290
Ser Leu Pro Asp His Glu Lys Gln Arg Arg Lys Asp Glu Thr Tyr Pro	
345 350 355	
att aag acc ccc acc ttt gca gga ggc ctt ttt tct ata tct aaa aaa	1338
Ile Lys Thr Pro Thr Phe Ala Gly Gly Leu Phe Ser Ile Ser Lys Lys	
360 365 370	
tat ttt gag cac att gga agt tac gat gaa gaa atg gaa atc tgg gga	1386
Tyr Phe Glu His Ile Gly Ser Tyr Asp Glu Glu Met Glu Ile Trp Gly	
375 380 385	
ggg gaa aat ata gaa atg tca ttc cga gtg tgg caa tgt ggt ggg cag	1434
Gly Glu Asn Ile Glu Met Ser Phe Arg Val Trp Gln Cys Gly Gly Gln	
390 395 400	
ttg gag att atg cct tgc tct gtt gtt gga cat gtt ttt cgc agc aaa	1482
Leu Glu Ile Met Pro Cys Ser Val Val Gly His Val Phe Arg Ser Lys	
405 410 415 420	
agc cct cat acc ttc cca aaa ggc acg cag gtg att gct cgt aac caa	1530
Ser Pro His Thr Phe Pro Lys Gly Thr Gln Val Ile Ala Arg Asn Gln	
425 430 435	
gtt cgc ctt gca gag gtc tgg atg gac gaa tac aag gaa ata ttt tat	1578
Val Arg Leu Ala Glu Val Trp Met Asp Glu Tyr Lys Glu Ile Phe Tyr	
440 445 450	
agg aga aac aca gat gca gca aaa atc gtt aag caa aaa tca ttt ggt	1626
Arg Arg Asn Thr Asp Ala Ala Lys Ile Val Lys Gln Lys Ser Phe Gly	
455 460 465	
gat ctt tcc aaa aga ttt gaa ata aag aaa cgc ctt cag tgt aaa aat	1674
Asp Leu Ser Lys Arg Phe Glu Ile Lys Lys Arg Leu Gln Cys Lys Asn	
470 475 480	
ttt acc tgg tac ctg aac act att tac ccg gaa gcg tat gtg cca gac	1722
Phe Thr Trp Tyr Leu Asn Thr Ile Tyr Pro Glu Ala Tyr Val Pro Asp	
485 490 495 500	
ctt aat cct gtt ata tct gga tat att aag agt gtg ggt caa cct tta	1770
Leu Asn Pro Val Ile Ser Gly Tyr Ile Lys Ser Val Gly Gln Pro Leu	
505 510 515	
tgt ctg gat gtt ggt gag aat aac cag gga ggc aaa cca ttg att ctg	1818
Cys Leu Asp Val Gly Glu Asn Asn Gln Gly Gly Lys Pro Leu Ile Leu	
520 525 530	
tac acg tgc cac ggc ctc ggg gga aat cag tac ttc gag tat tct gct	1866
Tyr Thr Cys His Gly Leu Gly Gly Asn Gln Tyr Phe Glu Tyr Ser Ala	
535 540 545	
cag cgt gaa atc cgg cac aac atc cag aag gag ctg tgt ctt cat gct	1914
Gln Arg Glu Ile Arg His Asn Ile Gln Lys Glu Leu Cys Leu His Ala	
550 555 560	

act cag ggt gtc gtc cag ctg aag gca tgt gtc tat aaa ggt cac agg	1962
Thr Gln Gly Val Val Gln Leu Lys Ala Cys Val Tyr Lys Gly His Arg	
565 570 575 580	
acc atc gcc cct gga gaa cag ata tgg gag att cgg aag gac caa ctt	2010
Thr Ile Ala Pro Gly Glu Gln Ile Trp Glu Ile Arg Lys Asp Gln Leu	
585 590 595	
cta tat aat cca tta ttt aaa atg tgc ctt tca tca aat gga gag cat	2058
Leu Tyr Asn Pro Leu Phe Lys Met Cys Leu Ser Ser Asn Gly Glu His	
600 605 610	
cca aac tta gtg cca tgt gac gca aca gat cta ctc caa aaa tgg att	2106
Pro Asn Leu Val Pro Cys Asp Ala Thr Asp Leu Leu Gln Lys Trp Ile	
615 620 625	
ttt agc caa aat gaa taa gtgttcctta aaattaagga gttgaaaagg	2154
Phe Ser Gln Asn Glu	
630	
acatactctt cctcataaaa ctgtgactag gcatacactg tagttgttga aaattatgca	2214
aaagcagcta attgtaactt attccaagtg catttcctta tttatatctt aagatgtcta	2274
tgtagaaccg ctgcagaaac cctgggggttt ctgtctgaaa gcacagcaac tagaatacca	2334
aagacgattc tgaaatgtcc agatgtagaa gagagatggt tacagtgtga agaaaataat	2394
ttccttagta aagtgaggtg tggttgtaca cttgggggatc tacacacctg catccacaca	2454
ctcacagctg aaaatgtttt ccctaatttt aggggcaata gaaaaagatt tgatactgta	2514
tttttataac tatatagaaa tggatcaatg aaggccagtc atttggcctt tcggtacaaa	2574
ccaggaactt tttatcgatc tagaattcat tgttttaaaa tccaggtaaa cttttgttgt	2634
ctcttgttga cttgtctgtc aaatatttcc ttaaacaatga agttgataag gagaggacta	2694
tttttaacat ttaaattttt ggaaaattta caaatatttt ttagaagccc actccacttg	2754
atgcacatga gtcttcccca aatagctttt ctgaagtgac tatactgtgt gttttctcag	2814
agtacttttt aaaaaataaa taaactttat aaattattag ctgttaaaaa aaaaaaaaaa	2874
aaaaa	2879

<210> 26
 <211> 633
 <212> PRT
 <213> Mouse

<400> 26

Met Ala His Leu Lys Arg Leu Val Lys Leu His Ile Lys Arg His Tyr
1 5 10 15

His Arg Lys Phe Trp Lys Leu Gly Ala Val Ile Phe Phe Phe Leu Val

20					25					30					
Val	Leu	Ile	Leu	Met	Gln	Arg	Glu	Val	Ser	Val	Gln	Tyr	Ser	Lys	Glu
	35						40					45			
Glu	Ser	Lys	Met	Glu	Arg	Asn	Leu	Lys	Asn	Lys	Asn	Lys	Met	Leu	Asp
	50					55					60				
Phe	Met	Leu	Glu	Ala	Val	Asn	Asn	Ile	Lys	Asp	Ala	Met	Pro	Lys	Met
	65					70					75				80
Gln	Ile	Gly	Ala	Pro	Ile	Lys	Glu	Asn	Ile	Asp	Val	Arg	Glu	Arg	Pro
				85					90					95	
Cys	Leu	Gln	Gly	Tyr	Tyr	Thr	Ala	Ala	Glu	Leu	Lys	Pro	Val	Phe	Asp
			100					105						110	
Arg	Pro	Pro	Gln	Asp	Ser	Asn	Ala	Pro	Gly	Ala	Ser	Gly	Lys	Pro	Phe
		115					120						125		
Lys	Ile	Thr	His	Leu	Ser	Pro	Glu	Glu	Gln	Lys	Glu	Lys	Glu	Arg	Gly
	130					135					140				
Glu	Thr	Lys	His	Cys	Phe	Asn	Ala	Phe	Ala	Ser	Asp	Arg	Ile	Ser	Leu
	145					150					155				160
His	Arg	Asp	Leu	Gly	Pro	Asp	Thr	Arg	Pro	Pro	Glu	Cys	Ile	Glu	Gln
				165					170					175	
Lys	Phe	Lys	Arg	Cys	Pro	Pro	Leu	Pro	Thr	Thr	Ser	Val	Ile	Ile	Val
			180					185						190	
Phe	His	Asn	Glu	Ala	Trp	Ser	Thr	Leu	Leu	Arg	Thr	Val	His	Ser	Val
		195					200					205			
Leu	Tyr	Ser	Ser	Pro	Ala	Ile	Leu	Leu	Lys	Glu	Ile	Ile	Leu	Val	Asp
	210					215					220				
Asp	Ala	Ser	Val	Asp	Asp	Tyr	Leu	His	Glu	Lys	Leu	Glu	Glu	Tyr	Ile
	225					230					235				240
Lys	Gln	Phe	Ser	Ile	Val	Lys	Ile	Val	Arg	Gln	Gln	Glu	Arg	Lys	Gly
				245					250					255	
Leu	Ile	Thr	Ala	Arg	Leu	Leu	Gly	Ala	Ala	Val	Ala	Thr	Ala	Glu	Thr

260					265					270					
Leu	Thr	Phe	Leu	Asp	Ala	His	Cys	Glu	Cys	Phe	Tyr	Gly	Trp	Leu	Glu
		275					280					285			
Pro	Leu	Leu	Ala	Arg	Ile	Ala	Glu	Asn	Tyr	Thr	Ala	Val	Val	Ser	Pro
	290					295					300				
Asp	Ile	Ala	Ser	Ile	Asp	Leu	Asn	Thr	Phe	Glu	Phe	Asn	Lys	Pro	Ser
305						310					315				320
Pro	Tyr	Gly	Ser	Asn	His	Asn	Arg	Gly	Asn	Phe	Asp	Trp	Ser	Leu	Ser
				325					330					335	
Phe	Gly	Trp	Glu	Ser	Leu	Pro	Asp	His	Glu	Lys	Gln	Arg	Arg	Lys	Asp
			340						345					350	
Glu	Thr	Tyr	Pro	Ile	Lys	Thr	Pro	Thr	Phe	Ala	Gly	Gly	Leu	Phe	Ser
		355					360						365		
Ile	Ser	Lys	Lys	Tyr	Phe	Glu	His	Ile	Gly	Ser	Tyr	Asp	Glu	Glu	Met
	370					375					380				
Glu	Ile	Trp	Gly	Gly	Glu	Asn	Ile	Glu	Met	Ser	Phe	Arg	Val	Trp	Gln
385						390					395				400
Cys	Gly	Gly	Gln	Leu	Glu	Ile	Met	Pro	Cys	Ser	Val	Val	Gly	His	Val
				405					410					415	
Phe	Arg	Ser	Lys	Ser	Pro	His	Thr	Phe	Pro	Lys	Gly	Thr	Gln	Val	Ile
			420					425					430		
Ala	Arg	Asn	Gln	Val	Arg	Leu	Ala	Glu	Val	Trp	Met	Asp	Glu	Tyr	Lys
		435					440					445			
Glu	Ile	Phe	Tyr	Arg	Arg	Asn	Thr	Asp	Ala	Ala	Lys	Ile	Val	Lys	Gln
	450					455					460				
Lys	Ser	Phe	Gly	Asp	Leu	Ser	Lys	Arg	Phe	Glu	Ile	Lys	Lys	Arg	Leu
465						470					475				480
Gln	Cys	Lys	Asn	Phe	Thr	Trp	Tyr	Leu	Asn	Thr	Ile	Tyr	Pro	Glu	Ala
				485					490					495	
Tyr	Val	Pro	Asp	Leu	Asn	Pro	Val	Ile	Ser	Gly	Tyr	Ile	Lys	Ser	Val

500								505				510				
Gly	Gln	Pro	Leu	Cys	Leu	Asp	Val	Gly	Glu	Asn	Asn	Gln	Gly	Gly	Lys	
515								520				525				
Pro	Leu	Ile	Leu	Tyr	Thr	Cys	His	Gly	Leu	Gly	Gly	Asn	Gln	Tyr	Phe	
530								535				540				
Glu	Tyr	Ser	Ala	Gln	Arg	Glu	Ile	Arg	His	Asn	Ile	Gln	Lys	Glu	Leu	
545								550				555				
Cys	Leu	His	Ala	Thr	Gln	Gly	Val	Val	Gln	Leu	Lys	Ala	Cys	Val	Tyr	
565								570				575				
Lys	Gly	His	Arg	Thr	Ile	Ala	Pro	Gly	Glu	Gln	Ile	Trp	Glu	Ile	Arg	
580								585				590				
Lys	Asp	Gln	Leu	Leu	Tyr	Asn	Pro	Leu	Phe	Lys	Met	Cys	Leu	Ser	Ser	
595								600				605				
Asn	Gly	Glu	His	Pro	Asn	Leu	Val	Pro	Cys	Asp	Ala	Thr	Asp	Leu	Leu	
610								615				620				
Gln	Lys	Trp	Ile	Phe	Ser	Gln	Asn	Glu								
625								630								

<210> 27
 <211> 5540
 <212> DNA
 <213> human

<220>
 <221> CDS
 <222> (144)..(1838)

<400> 27	
aattgcttcc ggggagttgc gagggagcga gggggaataa aggacccgcg aggaagggcc	60
cgcggatggc gcgtccctga gggtcgtggc gagttcgcg agcgtgggaa ggagcggacc	120
ctgctctccc cgggctgcg gcc atg gcc acg gcg gag cgg aga gcc ctc ggc	173
Met Ala Thr Ala Glu Arg Arg Ala Leu Gly	
1 5 10	
atc ggc ttc cag tgg ctc tct ttg gcc act ctg gtg ctc atc tgc gcc	221
Ile Gly Phe Gln Trp Leu Ser Leu Ala Thr Leu Val Leu Ile Cys Ala	
15 20 25	
ggg caa ggg gga cgc agg gag gat ggg ggt cca gcc tgc tac ggc gga	269
Gly Gln Gly Gly Arg Arg Glu Asp Gly Gly Pro Ala Cys Tyr Gly Gly	

30					35					40					
ttt gac ctg tac ttc att ttg gac aaa tca gga agt gtg ctg cac cac	317														
Phe Asp Leu Tyr Phe Ile Leu Asp Lys Ser Gly Ser Val Leu His His															
45 50 55															
tgg aat gaa atc tat tac ttt gtg gaa cag ttg gct cac aaa ttc atc	365														
Trp Asn Glu Ile Tyr Tyr Phe Val Glu Gln Leu Ala His Lys Phe Ile															
60 65 70															
agc cca cag ttg aga atg tcc ttt att gtt ttc tcc acc cga gga aca	413														
Ser Pro Gln Leu Arg Met Ser Phe Ile Val Phe Ser Thr Arg Gly Thr															
75 80 85 90															
acc tta atg aaa ctg aca gaa gac aga gaa caa atc cgt caa ggc cta	461														
Thr Leu Met Lys Leu Thr Glu Asp Arg Glu Gln Ile Arg Gln Gly Leu															
95 100 105															
gaa gaa ctc cag aaa gtt ctg cca gga gga gac act tac atg cat gaa	509														
Glu Glu Leu Gln Lys Val Leu Pro Gly Gly Asp Thr Tyr Met His Glu															
110 115 120															
gga ttt gaa agg gcc agt gag cag att tat tat gaa aac aga caa ggg	557														
Gly Phe Glu Arg Ala Ser Glu Gln Ile Tyr Tyr Glu Asn Arg Gln Gly															
125 130 135															
tac agg aca gcc agc gtc atc att gct ttg act gat gga gaa ctc cat	605														
Tyr Arg Thr Ala Ser Val Ile Ile Ala Leu Thr Asp Gly Glu Leu His															
140 145 150															
gaa gat ctc ttt ttc tat tca gag agg gag gct aat agg tct cga gat	653														
Glu Asp Leu Phe Phe Tyr Ser Glu Arg Glu Ala Asn Arg Ser Arg Asp															
155 160 165 170															
ctt ggt gca att gtt tac tgt gtt ggt gtg aaa gat ttc aat gag aca	701														
Leu Gly Ala Ile Val Tyr Cys Val Gly Val Lys Asp Phe Asn Glu Thr															
175 180 185															
cag ctg gcc cgg att gcg gac agt aag gat cat gtg ttt ccc gtg aat	749														
Gln Leu Ala Arg Ile Ala Asp Ser Lys Asp His Val Phe Pro Val Asn															
190 195 200															
gac ggc ttt cag gct ctg caa ggc atc atc cac tca att ttg aag aag	797														
Asp Gly Phe Gln Ala Leu Gln Gly Ile Ile His Ser Ile Leu Lys Lys															
205 210 215															
tcc tgc atc gaa att cta gca gct gaa cca tcc acc ata tgt gca gga	845														
Ser Cys Ile Glu Ile Leu Ala Ala Glu Pro Ser Thr Ile Cys Ala Gly															
220 225 230															
gag tca ttt caa gtt gtc gtg aga gga aac ggc ttc cga cat gcc cgc	893														
Glu Ser Phe Gln Val Val Val Arg Gly Asn Gly Phe Arg His Ala Arg															
235 240 245 250															
aac gtg gac agg gtc ctc tgc agc ttc aag atc aat gac tcg gtc aca	941														
Asn Val Asp Arg Val Leu Cys Ser Phe Lys Ile Asn Asp Ser Val Thr															
255 260 265															
ctc aat gag aag ccc ttt tct gtg gaa gat act tat tta ctg tgt cca	989														
Leu Asn Glu Lys Pro Phe Ser Val Glu Asp Thr Tyr Leu Leu Cys Pro															

270								275				280							
gcg	cct	atc	tta	aaa	gaa	gtt	ggc	atg	aaa	gct	gca	ctc	cag	gtc	agc		1037		
Ala	Pro	Ile	Leu	Lys	Glu	Val	Gly	Met	Lys	Ala	Ala	Leu	Gln	Val	Ser				
		285					290					295							
atg	aac	gat	ggc	ctc	tct	ttt	atc	tcc	agt	tct	gtc	atc	atc	acc	acc		1085		
Met	Asn	Asp	Gly	Leu	Ser	Phe	Ile	Ser	Ser	Ser	Val	Ile	Ile	Thr	Thr				
	300					305					310								
aca	cac	tgt	tct	gac	ggg	tcc	atc	ctg	gcc	atc	gcc	ctg	ctg	atc	ctg		1133		
Thr	His	Cys	Ser	Asp	Gly	Ser	Ile	Leu	Ala	Ile	Ala	Leu	Leu	Ile	Leu				
	315				320					325					330				
ttc	ctg	ctc	cta	gcc	ctg	gct	ctc	ctc	tgg	tgg	ttc	tgg	ccc	ctc	tgc		1181		
Phe	Leu	Leu	Leu	Ala	Leu	Ala	Leu	Leu	Trp	Trp	Phe	Trp	Pro	Leu	Cys				
				335					340					345					
tgc	act	gtg	att	atc	aag	gag	gtc	cct	cca	ccc	cct	gcc	gag	gag	agt		1229		
Cys	Thr	Val	Ile	Ile	Lys	Glu	Val	Pro	Pro	Pro	Pro	Ala	Glu	Glu	Ser				
			350					355					360						
gag	gaa	gaa	gat	gat	gat	ggg	ctg	cct	aag	aaa	aag	tgg	cca	acg	gta		1277		
Glu	Glu	Glu	Asp	Asp	Asp	Gly	Leu	Pro	Lys	Lys	Lys	Trp	Pro	Thr	Val				
		365					370					375							
gac	gcc	tct	tat	tat	ggg	ggg	aga	ggc	gtt	gga	ggc	att	aaa	aga	atg		1325		
Asp	Ala	Ser	Tyr	Tyr	Gly	Gly	Arg	Gly	Val	Gly	Gly	Ile	Lys	Arg	Met				
	380					385					390								
gag	gtt	cgt	tgg	gga	gaa	aag	ggc	tcc	aca	gaa	gaa	ggg	gct	aag	ttg		1373		
Glu	Val	Arg	Trp	Gly	Glu	Lys	Gly	Ser	Thr	Glu	Glu	Gly	Ala	Lys	Leu				
	395				400					405					410				
gaa	aag	gca	aag	aat	gca	aga	gtc	aag	atg	ccg	gag	cag	gaa	tat	gaa		1421		
Glu	Lys	Ala	Lys	Asn	Ala	Arg	Val	Lys	Met	Pro	Glu	Gln	Glu	Tyr	Glu				
				415					420				425						
ttc	cct	gag	ccg	cga	aat	ctc	aac	aac	aat	atg	cgt	cgg	cct	tct	tcc		1469		
Phe	Pro	Glu	Pro	Arg	Asn	Leu	Asn	Asn	Asn	Met	Arg	Arg	Pro	Ser	Ser				
			430					435					440						
ccc	cgg	aag	tgg	tac	tct	cca	atc	aag	gga	aaa	ctc	gat	gcc	ttg	tgg		1517		
Pro	Arg	Lys	Trp	Tyr	Ser	Pro	Ile	Lys	Gly	Lys	Leu	Asp	Ala	Leu	Trp				
		445					450					455							
gtc	cta	ctg	agg	aaa	gga	tat	gat	cgt	gtg	tct	gtg	atg	cgt	cca	cag		1565		
Val	Leu	Leu	Arg	Lys	Gly	Tyr	Asp	Arg	Val	Ser	Val	Met	Arg	Pro	Gln				
	460					465					470								
cca	gga	gac	acg	ggg	cgc	tgc	atc	aac	ttc	acc	agg	gtc	aag	aac	aac		1613		
Pro	Gly	Asp	Thr	Gly	Arg	Cys	Ile	Asn	Phe	Thr	Arg	Val	Lys	Asn	Asn				
	475				480					485					490				
cag	cca	gcc	aag	tac	cca	ctc	aac	aac	gcc	tac	cac	acc	tcc	tcg	ccg		1661		
Gln	Pro	Ala	Lys	Tyr	Pro	Leu	Asn	Asn	Ala	Tyr	His	Thr	Ser	Ser	Pro				
				495					500					505					
cct	cct	gcc	ccc	atc	tac	act	ccc	cca	cct	cct	gcg	ccc	cac	tgc	cct		1709		
Pro	Pro	Ala	Pro	Ile	Tyr	Thr	Pro	Pro	Pro	Pro	Ala	Pro	His	Cys	Pro				

510	515	520	
ccc ccg ccc ccc agc gcc cct acc cct ccc atc ccg tcc cca cct tcc Pro Pro Pro Pro Ser Ala Pro Thr Pro Pro Ile Pro Ser Pro Pro Ser 525 530 535			1757
acc ctt ccc cct cct ccc cag gct cca cct ccc aac agg gca cct cct Thr Leu Pro Pro Pro Pro Gln Ala Pro Pro Pro Asn Arg Ala Pro Pro 540 545 550			1805
ccc tcc cgc cct cct cca agg cct tct gtc tag agcccaaagt tcttgctctg Pro Ser Arg Pro Pro Arg Pro Ser Val 555 560			1858
ggctctctca gaaacttcag gagatggttag aacaagtctt tccagttaga gaagaggagt			1918
ggtgataaag cccactgacc ttcacacatt ctaaaaattg gttggcaatg ccagtatacc			1978
aacaatcatg atcagctgaa agaaacagat attttaaatt gccagaaaac aaatgatgag			2038
gcaactacag tcagatttat agccagccat ctatcacctc tagaaggttc cagagacagt			2098
gaaactgcaa gatgctctca acaggattat gtctcatgga gaccagtaag aaaatcattt			2158
atctgaaggt gaaatgcaga gttggataag aaatacattg ctgggtttct aaaatgctgc			2218
cttctgcct ctactccacc tccatccctg gactttggac ccttggccta ggagcctaag			2278
gaccttcacc cctgtgcacc acccaagaaa gaggaaaact ttgcctacaa ctttggaat			2338
gctgggggtcc ctgggtgtgt aagaaactca acatcagacg ggtatgcaga aggatgttct			2398
tctgggattt gcaggtagat aaaaaatgta tggcatcttt tccttgcaaa ttcttccagt			2458
ttccaagtga gaaggggagc aggtgtttac tgatggaaaa ggtatgttgc tatgttgatg			2518
tgtaagtga atcagttgtg tgcaatagac aggggcgtat tcatgggagc atcagccagt			2578
ttctaaaacc cacaggccat cagcagctag aggtggctgg ctttggccag acatggaccc			2638
taaatcaaca gacaatggca ttgtcgaaga gcaacctgtt aatgaatcat gttaaaaaatc			2698
aaggtttggc ttcagtttaa atcacttgag gtatgaagtt tatcctgttt tccagagata			2758
aacataagtt gatcttccca aaataccatc attaggacct atcacacaat atcactagtt			2818
ttttttgttt gtttgttttt tgtttttttt cttggtaaag ccatgcacca cagacttctg			2878
ggcagagctg agagacaatg gtcttgacat aataaggatc tttgattaac ccccataagg			2938
catgtgtgtg tatacaaata tacttctctt tggcttttctg acatagaacc tcagctgtta			2998
accaagggga aatacatcag atctgcaaca cagaaatgct ctgcctgaaa tttccaccat			3058
gcctaggact caccctattt atccaggtct ttctggatct gtttaaatcaa taagccctat			3118
aatcacttgc taaacactgg gcttcatcac ccagggataa aaacagagat cattgtcttg			3178
gacctcctgc atcagcctat tcaaaattat ctctctctct agctttccac aaatcctaaa			3238

attcctgtcc	caagccaccc	aaattctcag	atcttttctg	gaacaaggca	gaatataaaa	3298
taaatataca	tttagtggct	tgggctatgg	tctccaaaga	tccttcaaaa	atacatcaag	3358
ccagcttcat	tcactcactt	tacttagaac	agagatataa	gggcctggga	tgcattttatt	3418
ttatcaatac	caatttttgt	ggccatggca	gacattgcta	atcaatcaca	gcactatttc	3478
ctattaagcc	cactgatttc	ttcacaatcc	ttctcaaatt	acaattccaa	agagccgcca	3538
ctcaacagtc	agatgaaccc	aacagtcaga	tgagagaaat	gaaccctact	tgctatctct	3598
atcttagaaa	gcaaaaacaa	acaggagttt	ccagggagaa	tgggaaagcc	agggggcata	3658
aaagggtacag	tcaggggaaa	atagatctag	gcagagtgcc	ttagtcaggg	accacgggcg	3718
ctgaatctgc	agtgccaaca	ccaaactgac	acatctccag	gtgtacctcc	aaccctagcc	3778
ttctcccaca	gctgcctaca	acagagtctc	ccagccttct	cagagagcta	aaaccagaaa	3838
tttcagact	catgaaagca	acccccagc	ctctcccaa	ccctgccgca	ttgtctaatt	3898
tttagaacac	taggtttctt	ctttcatgta	gttcctcata	agcagggggc	agaatatctc	3958
agccacctgc	agtgacattg	ctggacccct	gaaaaccatt	ccataggaga	atgggttccc	4018
caggctcaca	gtgtagagac	attgagccca	tcacaactgt	tttgactgct	ggcagtctaa	4078
aacagtccac	ccaccccatg	gcactgccgc	gtgattcccc	cggccattca	gaagttcaag	4138
ccgagatgct	gacgttgctg	agcaacgaga	tgggtgagcat	cagtgcaaat	gcaccattca	4198
gcacatcagt	catatgccca	gtgcagttac	aagatgttgt	ttcggcaaag	cattttgatg	4258
gaatagggaa	ctgcaaattg	atgatgattt	tgaaaaggct	cagcaggatt	tgttcttaaa	4318
ccgactcagt	gtgtcatccc	cggttattta	gaattacagt	taagaaggag	aaacttctat	4378
aagactgtat	gaacaagggtg	atatcttcat	agtgggctat	tacaggcagg	aaaatgtttt	4438
aactggttta	caaaatccat	caatacttgt	gtcattccct	gtaaaaggca	ggagacatgt	4498
gattatgatc	aggaaactgc	acaaaattat	tgttttcagc	ccccgtgtta	ttgtcctttt	4558
gaactgtttt	ttttttatta	aagccaaatt	tgtgttgat	atattcgtat	tccatgtggt	4618
agatggaagc	atttcctatc	cagtgtgaat	aaaaagaaca	gttgtagtaa	attattataa	4678
agccgatgat	atttcattggc	aggttattct	accaagctgt	gcttgttggg	ttttcccatg	4738
actgtattgc	ttttataaat	gtacaaatag	ttactgaaat	gacgagaccc	ttgtttgcac	4798
agcattaata	agaaccttga	taagaaccat	attctgttga	cagccagctc	acagtttctt	4858
gcctgaagct	tgggtgcaccc	tccagtgaga	cacaagatct	ctcttttacc	aaagttgaga	4918
acagagctgg	tggattaatt	aatagtcttc	gatatctggc	catgggtaac	ctcattgtaa	4978
ctatcatcag	aatgggcaga	gatgatcttg	aagtgtcaca	tacactaaag	tccaaacact	5038

atgtcagatg ggggtaaaat ccattaaaga acaggaaaaa ataattataa gatgataagc 5098
 aaatgtttca gcccaatgtc aaccagttta aaaaaaaaat taatgctgtg taaaatgggt 5158
 gaattagttt gcaaactata taaagacata tgcagtaaaa agtctgttaa tgcacatcct 5218
 gtgggaatgg agtgttctaa ccaattgcct tttcttggtta tctgagctct cctatattat 5278
 catactcaga taaccaaatt aaaagaatta gaatatgatt ttaatacac ttaacattaa 5338
 actcttctaa ctttcttctt tctgtgataa ttcagaagat agttatggat cttcaatgcc 5398
 tctgagtcac tgttataaaa aatcagttat cactatacca tgctatagga gactgggcaa 5458
 aacctgtaca atgacaaccc tggaagttgc tttttttaa aaaataataa atttcttaaa 5518
 tcaaaaaaaaa aaaaaaaaaa aa 5540

<210> 28
 <211> 564
 <212> PRT
 <213> human

<400> 28

Met Ala Thr Ala Glu Arg Arg Ala Leu Gly Ile Gly Phe Gln Trp Leu
 1 5 10 15

Ser Leu Ala Thr Leu Val Leu Ile Cys Ala Gly Gln Gly Gly Arg Arg
 20 25 30

Glu Asp Gly Gly Pro Ala Cys Tyr Gly Gly Phe Asp Leu Tyr Phe Ile
 35 40 45

Leu Asp Lys Ser Gly Ser Val Leu His His Trp Asn Glu Ile Tyr Tyr
 50 55 60

Phe Val Glu Gln Leu Ala His Lys Phe Ile Ser Pro Gln Leu Arg Met
 65 70 75 80

Ser Phe Ile Val Phe Ser Thr Arg Gly Thr Thr Leu Met Lys Leu Thr
 85 90 95

Glu Asp Arg Glu Gln Ile Arg Gln Gly Leu Glu Glu Leu Gln Lys Val
 100 105 110

Leu Pro Gly Gly Asp Thr Tyr Met His Glu Gly Phe Glu Arg Ala Ser
 115 120 125

Glu Gln Ile Tyr Tyr Glu Asn Arg Gln Gly Tyr Arg Thr Ala Ser Val
 130 135 140

Ile	Ile	Ala	Leu	Thr	Asp	Gly	Glu	Leu	His	Glu	Asp	Leu	Phe	Phe	Tyr	145	150	155	160
Ser	Glu	Arg	Glu	Ala	Asn	Arg	Ser	Arg	Asp	Leu	Gly	Ala	Ile	Val	Tyr	165	170	175	
Cys	Val	Gly	Val	Lys	Asp	Phe	Asn	Glu	Thr	Gln	Leu	Ala	Arg	Ile	Ala	180	185	190	
Asp	Ser	Lys	Asp	His	Val	Phe	Pro	Val	Asn	Asp	Gly	Phe	Gln	Ala	Leu	195	200	205	
Gln	Gly	Ile	Ile	His	Ser	Ile	Leu	Lys	Lys	Ser	Cys	Ile	Glu	Ile	Leu	210	215	220	
Ala	Ala	Glu	Pro	Ser	Thr	Ile	Cys	Ala	Gly	Glu	Ser	Phe	Gln	Val	Val	225	230	235	240
Val	Arg	Gly	Asn	Gly	Phe	Arg	His	Ala	Arg	Asn	Val	Asp	Arg	Val	Leu	245	250	255	
Cys	Ser	Phe	Lys	Ile	Asn	Asp	Ser	Val	Thr	Leu	Asn	Glu	Lys	Pro	Phe	260	265	270	
Ser	Val	Glu	Asp	Thr	Tyr	Leu	Leu	Cys	Pro	Ala	Pro	Ile	Leu	Lys	Glu	275	280	285	
Val	Gly	Met	Lys	Ala	Ala	Leu	Gln	Val	Ser	Met	Asn	Asp	Gly	Leu	Ser	290	295	300	
Phe	Ile	Ser	Ser	Ser	Val	Ile	Ile	Thr	Thr	Thr	His	Cys	Ser	Asp	Gly	305	310	315	320
Ser	Ile	Leu	Ala	Ile	Ala	Leu	Leu	Ile	Leu	Phe	Leu	Leu	Leu	Ala	Leu	325	330	335	
Ala	Leu	Leu	Trp	Trp	Phe	Trp	Pro	Leu	Cys	Cys	Thr	Val	Ile	Ile	Lys	340	345	350	
Glu	Val	Pro	Pro	Pro	Pro	Ala	Glu	Glu	Ser	Glu	Glu	Glu	Asp	Asp	Asp	355	360	365	
Gly	Leu	Pro	Lys	Lys	Lys	Trp	Pro	Thr	Val	Asp	Ala	Ser	Tyr	Tyr	Gly	370	375	380	

Gly Arg Gly Val Gly Gly Ile Lys Arg Met Glu Val Arg Trp Gly Glu
385 390 395 400

Lys Gly Ser Thr Glu Glu Gly Ala Lys Leu Glu Lys Ala Lys Asn Ala
405 410 415

Arg Val Lys Met Pro Glu Gln Glu Tyr Glu Phe Pro Glu Pro Arg Asn
420 425 430

Leu Asn Asn Asn Met Arg Arg Pro Ser Ser Pro Arg Lys Trp Tyr Ser
435 440 445

Pro Ile Lys Gly Lys Leu Asp Ala Leu Trp Val Leu Leu Arg Lys Gly
450 455 460

Tyr Asp Arg Val Ser Val Met Arg Pro Gln Pro Gly Asp Thr Gly Arg
465 470 475 480

Cys Ile Asn Phe Thr Arg Val Lys Asn Asn Gln Pro Ala Lys Tyr Pro
485 490 495

Leu Asn Asn Ala Tyr His Thr Ser Ser Pro Pro Pro Ala Pro Ile Tyr
500 505 510

Thr Pro Pro Pro Pro Ala Pro His Cys Pro Pro Pro Pro Pro Ser Ala
515 520 525

Pro Thr Pro Pro Ile Pro Ser Pro Pro Ser Thr Leu Pro Pro Pro Pro
530 535 540

Gln Ala Pro Pro Pro Asn Arg Ala Pro Pro Pro Ser Arg Pro Pro Pro
545 550 555 560

Arg Pro Ser Val

<210> 29
<211> 1433
<212> DNA
<213> human

<220>
<221> CDS
<222> (148)..(900)

<400> 29
tgtgtgtgtg tgtgtgtgag cgcgcgcgcg cgcgcgcgtg tgtactcgtg cgtgtgcctg 60
tgtgtgcctg ggagtgacct cacagctgcc ggaacataaa gactcacagg tccgcctccc 120
aggctcaaag ctggctctgc aggggac atg aga ggc aca ccg aag acc cac ctc 174
Met Arg Gly Thr Pro Lys Thr His Leu
1 5
ctg gcc ttc tcc ctc ctc tgc ctc ctc tca aag gtg cgt acc cag ctg 222
Leu Ala Phe Ser Leu Leu Cys Leu Leu Ser Lys Val Arg Thr Gln Leu
10 15 20 25
tgc ccg aca cca tgt acc tgc ccc tgg cca cct ccc cga tgc ccg ctg 270
Cys Pro Thr Pro Cys Thr Cys Pro Trp Pro Pro Pro Arg Cys Pro Leu
30 35 40
gga gta ccc ctg gtg ctg gat ggc tgt ggc tgc tgc cgg gta tgt gca 318
Gly Val Pro Leu Val Leu Asp Gly Cys Gly Cys Cys Arg Val Cys Ala
45 50 55
cgg cgg ctg ggg gag ccc tgc gac caa ctc cac gtc tgc gac gcc agc 366
Arg Arg Leu Gly Glu Pro Cys Asp Gln Leu His Val Cys Asp Ala Ser
60 65 70
cag ggc ctg gtc tgc cag ccc ggg gca gga ccc ggt ggc cgg ggg gcc 414
Gln Gly Leu Val Cys Gln Pro Gly Ala Gly Pro Gly Gly Arg Gly Ala
75 80 85
ctg tgc ctc ttg gca gag gac gac agc agc tgt gag gtg aac ggc cgc 462
Leu Cys Leu Leu Ala Glu Asp Asp Ser Ser Cys Glu Val Asn Gly Arg
90 95 100 105
ctg tat cgg gaa ggg gag acc ttc cag ccc cac tgc agc atc cgc tgc 510
Leu Tyr Arg Glu Gly Glu Thr Phe Gln Pro His Cys Ser Ile Arg Cys
110 115 120
cgc tgc gag gac ggc ggc ttc acc tgc gtg ccg ctg tgc agc gag gat 558
Arg Cys Glu Asp Gly Gly Phe Thr Cys Val Pro Leu Cys Ser Glu Asp
125 130 135
gtg cgg ctg ccc agc tgg gac tgc ccc cac ccc agg agg gtc gag gtc 606
Val Arg Leu Pro Ser Trp Asp Cys Pro His Pro Arg Arg Val Glu Val
140 145 150
ctg ggc aag tgc tgc cct gag tgg gtg tgc ggc caa gga ggg gga ctg 654
Leu Gly Lys Cys Cys Pro Glu Trp Val Cys Gly Gln Gly Gly Gly Leu
155 160 165
ggg acc cag ccc ctt cca gcc caa gga ccc cag ttt tct ggc ctt gtc 702
Gly Thr Gln Pro Leu Pro Ala Gln Gly Pro Gln Phe Ser Gly Leu Val
170 175 180 185
tct tcc ctg ccc cct ggt gtc ccc tgc cca gaa tgg agc acg gcc tgg 750
Ser Ser Leu Pro Pro Gly Val Pro Cys Pro Glu Trp Ser Thr Ala Trp
190 195 200
gga ccc tgc tcg acc acc tgt ggg ctg ggc atg gcc acc cgg gtg tcc 798
Gly Pro Cys Ser Thr Thr Cys Gly Leu Gly Met Ala Thr Arg Val Ser
205 210 215

aac cag aac cgc ttc tgc cga ctg gag acc cag cgc cgc ctg tgc ctg	846
Asn Gln Asn Arg Phe Cys Arg Leu Glu Thr Gln Arg Arg Leu Cys Leu	
220 225 230	
tcc agg ccc tgc cca ccc tcc agg ggt cgc agt cca caa aac agt gcc	894
Ser Arg Pro Cys Pro Pro Ser Arg Gly Arg Ser Pro Gln Asn Ser Ala	
235 240 245	
ttc tag agccgggctg ggaatgggga cacgggtgtcc accatcccca gctggtggcc	950
Phe	
250	
ctgtgcctgg gccctgggct gatggaagat ggtccgtgcc caggcccttg gctgcaggca	1010
acacttttagc ttgggtccac catgcagaac accaatatta acacgctgcc tggctctgtct	1070
ggatccccgag gtatggcaga ggtgcaagac ctagtccccct ttcctctaac tcaactgccta	1130
ggaggctggc caaggtgtcc agggctcctct agcccactcc ctgcctacac acacagccta	1190
tatcaaacat gcacacgggc gagctttctc tccgacttcc cctgggcaag agatgggaca	1250
agcagtcctt taatattgag gctgcagcag gtgctgggct ggactggcca tttttctggg	1310
ggtaggatga agagaaggca cacagagatt ctggatctcc tgctgccttt tctggagttt	1370
gtaaaattgt tcctgaatac aagcctatgc gtgaaaaaaaa aaaaaaaaaa aaaaaaaaaa	1430
aaa	1433

<210> 30
 <211> 250
 <212> PRT
 <213> human

<400> 30

Met Arg Gly Thr Pro Lys Thr His Leu Leu Ala Phe Ser Leu Leu Cys
1 5 10 15

Leu Leu Ser Lys Val Arg Thr Gln Leu Cys Pro Thr Pro Cys Thr Cys
20 25 30

Pro Trp Pro Pro Pro Arg Cys Pro Leu Gly Val Pro Leu Val Leu Asp
35 40 45

Gly Cys Gly Cys Cys Arg Val Cys Ala Arg Arg Leu Gly Glu Pro Cys
50 55 60

Asp Gln Leu His Val Cys Asp Ala Ser Gln Gly Leu Val Cys Gln Pro
65 70 75 80

Gly Ala Gly Pro Gly Gly Arg Gly Ala Leu Cys Leu Leu Ala Glu Asp

85								90				95			
Asp	Ser	Ser	Cys	Glu	Val	Asn	Gly	Arg	Leu	Tyr	Arg	Glu	Gly	Glu	Thr
			100					105					110		
Phe	Gln	Pro	His	Cys	Ser	Ile	Arg	Cys	Arg	Cys	Glu	Asp	Gly	Gly	Phe
		115					120					125			
Thr	Cys	Val	Pro	Leu	Cys	Ser	Glu	Asp	Val	Arg	Leu	Pro	Ser	Trp	Asp
	130					135					140				
Cys	Pro	His	Pro	Arg	Arg	Val	Glu	Val	Leu	Gly	Lys	Cys	Cys	Pro	Glu
145					150					155					160
Trp	Val	Cys	Gly	Gln	Gly	Gly	Gly	Leu	Gly	Thr	Gln	Pro	Leu	Pro	Ala
				165					170						175
Gln	Gly	Pro	Gln	Phe	Ser	Gly	Leu	Val	Ser	Ser	Leu	Pro	Pro	Gly	Val
			180					185					190		
Pro	Cys	Pro	Glu	Trp	Ser	Thr	Ala	Trp	Gly	Pro	Cys	Ser	Thr	Thr	Cys
		195					200					205			
Gly	Leu	Gly	Met	Ala	Thr	Arg	Val	Ser	Asn	Gln	Asn	Arg	Phe	Cys	Arg
	210					215					220				
Leu	Glu	Thr	Gln	Arg	Arg	Leu	Cys	Leu	Ser	Arg	Pro	Cys	Pro	Pro	Ser
225					230					235					240
Arg	Gly	Arg	Ser	Pro	Gln	Asn	Ser	Ala	Phe						
				245					250						

<210> 31
 <211> 2502
 <212> DNA
 <213> human

<220>
 <221> CDS
 <222> (55)..(2154)

<400> 31
 gaattcgtgg gtcgtgctgc gtcgacaacg gtagtgacgc gtattgcctg gagg atg 57
 Met
 1

gcg gac gcc ggc att cgc cgc gtg gtt ccc agc gac ctg tat ccc ctc 105
 Ala Asp Ala Gly Ile Arg Arg Val Val Pro Ser Asp Leu Tyr Pro Leu

5					10					15						
gtg	ctc	ggc	ttc	ctg	cgc	gat	aac	caa	ctc	tca	gag	gtg	gcc	aat	aag	153
Val	Leu	Gly	Phe	Leu	Arg	Asp	Asn	Gln	Leu	Ser	Glu	Val	Ala	Asn	Lys	
		20					25					30				
ttc	gcc	aaa	gcg	aca	gga	gct	aca	cag	cag	gat	gcc	aat	gcc	tct	tcc	201
Phe	Ala	Lys	Ala	Thr	Gly	Ala	Thr	Gln	Gln	Asp	Ala	Asn	Ala	Ser	Ser	
	35					40					45					
ctc	tta	gac	atc	tat	agc	ttc	tgg	ctc	aag	tct	gcc	aag	gtc	cca	gag	249
Leu	Leu	Asp	Ile	Tyr	Ser	Phe	Trp	Leu	Lys	Ser	Ala	Lys	Val	Pro	Glu	
50					55					60					65	
cga	aag	tta	cag	gca	aat	gga	cca	gtg	gct	aag	aaa	gct	aag	aag	aag	297
Arg	Lys	Leu	Gln	Ala	Asn	Gly	Pro	Val	Ala	Lys	Lys	Ala	Lys	Lys	Lys	
			70						75						80	
gcc	tca	tcc	agt	gac	agt	gag	gac	agc	agc	gag	gag	gag	gag	gaa	gtt	345
Ala	Ser	Ser	Ser	Asp	Ser	Glu	Asp	Ser	Ser	Glu	Glu	Glu	Glu	Glu	Val	
			85					90					95			
caa	ggg	cct	cca	gca	aag	aag	gct	gct	gta	cct	gcc	aag	cga	gtc	ggt	393
Gln	Gly	Pro	Pro	Ala	Lys	Lys	Ala	Ala	Val	Pro	Ala	Lys	Arg	Val	Gly	
		100					105					110				
ctg	cct	cct	ggg	aag	gct	gca	gcc	aaa	gca	tca	gag	agt	agc	agc	agt	441
Leu	Pro	Pro	Gly	Lys	Ala	Ala	Ala	Lys	Ala	Ser	Glu	Ser	Ser	Ser	Ser	
	115					120					125					
gaa	gag	tcc	aga	gat	gat	gat	gat	gag	gag	gac	caa	aag	aaa	cag	cct	489
Glu	Glu	Ser	Arg	Asp	Asp	Asp	Asp	Glu	Glu	Asp	Gln	Lys	Lys	Gln	Pro	
130					135					140					145	
gtc	cag	aag	gga	gtt	aag	ccc	caa	gcc	aag	gca	gcc	aaa	gct	cct	cct	537
Val	Gln	Lys	Gly	Val	Lys	Pro	Gln	Ala	Lys	Ala	Ala	Lys	Ala	Pro	Pro	
				150				155						160		
aag	aag	gcc	aag	agc	tct	gat	tct	gat	tct	gac	tca	agc	tcc	gag	gat	585
Lys	Lys	Ala	Lys	Ser	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Ser	Ser	Ser	Asp	
			165					170						175		
gag	cca	cca	aag	aac	cag	aag	cca	aag	ata	aca	cct	gtg	aca	gtt	aaa	633
Glu	Pro	Pro	Lys	Asn	Gln	Lys	Pro	Lys	Ile	Thr	Pro	Val	Thr	Val	Lys	
		180					185					190				
gct	cag	act	aaa	gcc	cct	ccc	aaa	cca	gct	cga	gca	gca	cct	aaa	ata	681
Ala	Gln	Thr	Lys	Ala	Pro	Pro	Lys	Pro	Ala	Arg	Ala	Ala	Pro	Lys	Ile	
	195					200					205					
gcc	aat	ggt	aaa	gca	gcc	agt	agc	agc	agt	agc	agc	agc	agc	agc	agt	729
Ala	Asn	Gly	Lys	Ala	Ala	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	
210					215					220					225	
agc	agt	gat	gac	tca	gag	gag	gag	aag	gca	gca	gcc	acc	ccc	aag	aag	777
Ser	Ser	Asp	Asp	Ser	Glu	Glu	Glu	Lys	Ala	Ala	Ala	Thr	Pro	Lys	Lys	
				230				235						240		
act	gta	cct	aaa	aag	caa	gtt	gtg	gcc	aaa	gcc	cca	gtg	aaa	gca	gct	825
Thr	Val	Pro	Lys	Lys	Gln	Val	Val	Ala	Lys	Ala	Pro	Val	Lys	Ala	Ala	

245							250							255							
acc	acc	cct	acc	cgg	aag	agt	tct	agc	agt	gag	gat	tcc	tcc	agt	gac	873					
Thr	Thr	Pro	Thr	Arg	Lys	Ser	Ser	Ser	Ser	Glu	Asp	Ser	Ser	Ser	Asp						
		260					265					270									
gag	gaa	gag	gag	caa	aaa	aaa	ccc	atg	aaa	aat	aaa	cca	ggt	ccc	tac	921					
Glu	Glu	Glu	Glu	Gln	Lys	Lys	Pro	Met	Lys	Asn	Lys	Pro	Gly	Pro	Tyr						
	275					280					285										
agt	tac	gcc	ccc	ccg	cct	tct	gct	ccc	cca	cca	aag	aag	tct	ctg	gga	969					
Ser	Tyr	Ala	Pro	Pro	Pro	Ser	Ala	Pro	Pro	Pro	Lys	Lys	Ser	Leu	Gly						
290					295					300					305						
acc	cag	cct	ccc	aag	aag	gct	gtg	gag	aag	cag	cag	cct	gtg	gaa	agc	1017					
Thr	Gln	Pro	Pro	Lys	Lys	Ala	Val	Glu	Lys	Gln	Gln	Pro	Val	Glu	Ser						
				310					315					320							
agt	gaa	gac	agc	agt	gat	gag	tct	gat	tca	agt	tct	gaa	gaa	gag	aag	1065					
Ser	Glu	Asp	Ser	Ser	Asp	Glu	Ser	Asp	Ser	Ser	Ser	Glu	Glu	Glu	Lys						
			325					330					335								
aaa	ccc	cca	act	aag	gca	gta	gtc	tct	aaa	gca	acc	act	aaa	cca	cct	1113					
Lys	Pro	Pro	Thr	Lys	Ala	Val	Val	Ser	Lys	Ala	Thr	Thr	Lys	Pro	Pro						
		340					345						350								
cca	gca	aag	aaa	gca	gca	gag	agc	tct	tca	gac	agc	tca	gac	tct	gac	1161					
Pro	Ala	Lys	Lys	Ala	Ala	Glu	Ser	Ser	Ser	Asp	Ser	Ser	Asp	Ser	Asp						
	355					360					365										
agc	tct	gag	gat	gat	gaa	gct	cct	tct	aag	cca	gct	ggt	acc	acc	aag	1209					
Ser	Ser	Glu	Asp	Asp	Glu	Ala	Pro	Ser	Lys	Pro	Ala	Gly	Thr	Thr	Lys						
370					375					380					385						
aat	tct	tca	aat	aag	cca	gct	gtc	acc	acc	aag	tca	cct	gca	gtg	aag	1257					
Asn	Ser	Ser	Asn	Lys	Pro	Ala	Val	Thr	Thr	Lys	Ser	Pro	Ala	Val	Lys						
				390					395					400							
cca	gct	gca	gcc	ccc	aag	caa	cct	gtg	ggc	ggt	ggc	cag	aag	ctt	ctg	1305					
Pro	Ala	Ala	Ala	Pro	Lys	Gln	Pro	Val	Gly	Gly	Gly	Gln	Lys	Leu	Leu						
			405					410					415								
acg	aga	aag	gct	gac	agc	agc	tcc	agc	gag	gaa	gag	agc	agc	tcc	agt	1353					
Thr	Arg	Lys	Ala	Asp	Ser	Ser	Ser	Ser	Glu	Glu	Glu	Ser	Ser	Ser	Ser						
		420					425					430									
gag	gag	gag	aag	aca	aag	aag	atg	gtg	gcc	acc	act	aag	ccc	aag	gcg	1401					
Glu	Glu	Glu	Lys	Thr	Lys	Lys	Met	Val	Ala	Thr	Thr	Lys	Pro	Lys	Ala						
	435					440					445										
act	gcc	aaa	gca	gct	cta	tct	ctg	cct	gcc	aag	cag	gct	cct	cag	ggt	1449					
Thr	Ala	Lys	Ala	Ala	Leu	Ser	Leu	Pro	Ala	Lys	Gln	Ala	Pro	Gln	Gly						
450					455					460					465						
agt	agg	gac	agc	agc	tct	gat	tca	gac	agc	tcc	agc	agt	gag	gag	gag	1497					
Ser	Arg	Asp	Ser	Ser	Ser	Asp	Ser	Asp	Ser	Ser	Ser	Ser	Glu	Glu	Glu						
				470					475					480							
gaa	gag	aag	aca	tct	aag	tct	gca	gtt	aag	aag	aag	cca	cag	aag	gta	1545					
Glu	Glu	Lys	Thr	Ser	Lys	Ser	Ala	Val	Lys	Lys	Lys	Pro	Gln	Lys	Val						

485	490	495	
gca gga ggt gca gcc cct tcc aag cca gcc tct gca aag aaa gga aag Ala Gly Gly Ala Ala Pro Ser Lys Pro Ala Ser Ala Lys Lys Gly Lys 500 505 510			1593
gct gag agc agc aac agt tct tct tct gat gac tcc agt gag gaa gag Ala Glu Ser Ser Asn Ser Ser Ser Ser Asp Asp Ser Ser Glu Glu Glu 515 520 525			1641
gaa gag aag ctc aag ggc aag ggc tct cca aga cca caa gcc ccc aag Glu Glu Lys Leu Lys Gly Lys Gly Ser Pro Arg Pro Gln Ala Pro Lys 530 535 540 545			1689
gcc aat ggc acc tct gca ctg act gcc cag aat gga aaa gca gct aag Ala Asn Gly Thr Ser Ala Leu Thr Ala Gln Asn Gly Lys Ala Ala Lys 550 555 560			1737
aac agt gag gag gag gaa gaa gaa aag aaa aag gcg gca gtg gta gtt Asn Ser Glu Glu Glu Glu Glu Glu Lys Lys Lys Ala Ala Val Val Val 565 570 575			1785
tcc aaa tca ggt tca tta aag aag cgg aag cag aat gag gct gcc aag Ser Lys Ser Gly Ser Leu Lys Lys Arg Lys Gln Asn Glu Ala Ala Lys 580 585 590			1833
gag gca gag act cct cag gcc aag aag ata aag ctt cag acc cct aac Glu Ala Glu Thr Pro Gln Ala Lys Lys Ile Lys Leu Gln Thr Pro Asn 595 600 605			1881
aca ttt cca aaa agg aag aaa gga gaa aaa agg gca tca tcc cca ttc Thr Phe Pro Lys Arg Lys Lys Gly Glu Lys Arg Ala Ser Ser Pro Phe 610 615 620 625			1929
cga agg gtc agg gag gag gaa att gag gtg gat tca cga gtt gcg gac Arg Arg Val Arg Glu Glu Glu Ile Glu Val Asp Ser Arg Val Ala Asp 630 635 640			1977
aac tcc ttt gat gcc aag cga ggt gca gcc gga gac tgg gga gag cga Asn Ser Phe Asp Ala Lys Arg Gly Ala Ala Gly Asp Trp Gly Glu Arg 645 650 655			2025
gcc aat cag gtt ttg aag ttc acc aaa ggc aag tcc ttt cgg cat gag Ala Asn Gln Val Leu Lys Phe Thr Lys Gly Lys Ser Phe Arg His Glu 660 665 670			2073
aaa acc aag aag aag cgg ggc agc tac cgg gga ggc tca atc tct gtc Lys Thr Lys Lys Lys Arg Gly Ser Tyr Arg Gly Gly Ser Ile Ser Val 675 680 685			2121
cag gtc aat tct att aag ttt gac agc gag tga cctgaggcca tcttcggtga Gln Val Asn Ser Ile Lys Phe Asp Ser Glu			2174 690 695
agcaaggggtg atgatcggag actacttact ttctccagtg gacctgggaa ccctcaggtc			2234
tctaggtgag ggtcttgatg aggacagaag tttagagtag gtcctaagac tttacagtgt			2294
aacatcctct ctggtccttt tctgtgttcc tagttttgta cagacttggt tttgagtgtt			2354

gagtagcagg gacaaaataa gggaatgtta ttttttaaga aaattcattt tcattgttgt 2414
 ctcttcctt ttctgtgaaa gtcctcatat tgagaaattt gtatatattta tattaaatca 2474
 cttactattg aaaaaaaaaa aggaattc 2502

<210> 32
 <211> 699
 <212> PRT
 <213> human

<400> 32

Met Ala Asp Ala Gly Ile Arg Arg Val Val Pro Ser Asp Leu Tyr Pro
 1 5 10 15

Leu Val Leu Gly Phe Leu Arg Asp Asn Gln Leu Ser Glu Val Ala Asn
 20 25 30

Lys Phe Ala Lys Ala Thr Gly Ala Thr Gln Gln Asp Ala Asn Ala Ser
 35 40 45

Ser Leu Leu Asp Ile Tyr Ser Phe Trp Leu Lys Ser Ala Lys Val Pro
 50 55 60

Glu Arg Lys Leu Gln Ala Asn Gly Pro Val Ala Lys Lys Ala Lys Lys
 65 70 75 80

Lys Ala Ser Ser Ser Asp Ser Glu Asp Ser Ser Glu Glu Glu Glu Glu
 85 90 95

Val Gln Gly Pro Pro Ala Lys Lys Ala Ala Val Pro Ala Lys Arg Val
 100 105 110

Gly Leu Pro Pro Gly Lys Ala Ala Ala Lys Ala Ser Glu Ser Ser Ser
 115 120 125

Ser Glu Glu Ser Arg Asp Asp Asp Asp Glu Glu Asp Gln Lys Lys Gln
 130 135 140

Pro Val Gln Lys Gly Val Lys Pro Gln Ala Lys Ala Ala Lys Ala Pro
 145 150 155 160

Pro Lys Lys Ala Lys Ser Ser Asp Ser Asp Ser Asp Ser Ser Ser Glu
 165 170 175

Asp Glu Pro Pro Lys Asn Gln Lys Pro Lys Ile Thr Pro Val Thr Val
 180 185 190

Lys Ala Gln Thr Lys Ala Pro Pro Lys Pro Ala Arg Ala Ala Pro Lys
 195 200 205

Ile Ala Asn Gly Lys Ala Ala Ser Ser Ser Ser Ser Ser Ser Ser Ser
 210 215 220

Ser Ser Ser Asp Asp Ser Glu Glu Glu Lys Ala Ala Ala Thr Pro Lys
 225 230 235 240

Lys Thr Val Pro Lys Lys Gln Val Val Ala Lys Ala Pro Val Lys Ala
 245 250 255

Ala Thr Thr Pro Thr Arg Lys Ser Ser Ser Ser Glu Asp Ser Ser Ser
 260 265 270

Asp Glu Glu Glu Glu Gln Lys Lys Pro Met Lys Asn Lys Pro Gly Pro
 275 280 285

Tyr Ser Tyr Ala Pro Pro Pro Ser Ala Pro Pro Pro Lys Lys Ser Leu
 290 295 300

Gly Thr Gln Pro Pro Lys Lys Ala Val Glu Lys Gln Gln Pro Val Glu
 305 310 315 320

Ser Ser Glu Asp Ser Ser Asp Glu Ser Asp Ser Ser Ser Glu Glu Glu
 325 330 335

Lys Lys Pro Pro Thr Lys Ala Val Val Ser Lys Ala Thr Thr Lys Pro
 340 345 350

Pro Pro Ala Lys Lys Ala Ala Glu Ser Ser Ser Asp Ser Ser Asp Ser
 355 360 365

Asp Ser Ser Glu Asp Asp Glu Ala Pro Ser Lys Pro Ala Gly Thr Thr
 370 375 380

Lys Asn Ser Ser Asn Lys Pro Ala Val Thr Thr Lys Ser Pro Ala Val
 385 390 395 400

Lys Pro Ala Ala Ala Pro Lys Gln Pro Val Gly Gly Gly Gln Lys Leu
 405 410 415

Leu Thr Arg Lys Ala Asp Ser Ser Ser Ser Glu Glu Glu Ser Ser Ser
 420 425 430

Ser Glu Glu Glu Lys Thr Lys Lys Met Val Ala Thr Thr Lys Pro Lys
435 440 445

Ala Thr Ala Lys Ala Ala Leu Ser Leu Pro Ala Lys Gln Ala Pro Gln
450 455 460

Gly Ser Arg Asp Ser Ser Ser Asp Ser Asp Ser Ser Ser Ser Glu Glu
465 470 475 480

Glu Glu Glu Lys Thr Ser Lys Ser Ala Val Lys Lys Lys Pro Gln Lys
485 490 495

Val Ala Gly Gly Ala Ala Pro Ser Lys Pro Ala Ser Ala Lys Lys Gly
500 505 510

Lys Ala Glu Ser Ser Asn Ser Ser Ser Ser Asp Asp Ser Ser Glu Glu
515 520 525

Glu Glu Glu Lys Leu Lys Gly Lys Gly Ser Pro Arg Pro Gln Ala Pro
530 535 540

Lys Ala Asn Gly Thr Ser Ala Leu Thr Ala Gln Asn Gly Lys Ala Ala
545 550 555 560

Lys Asn Ser Glu Glu Glu Glu Glu Glu Lys Lys Lys Ala Ala Val Val
565 570 575

Val Ser Lys Ser Gly Ser Leu Lys Lys Arg Lys Gln Asn Glu Ala Ala
580 585 590

Lys Glu Ala Glu Thr Pro Gln Ala Lys Lys Ile Lys Leu Gln Thr Pro
595 600 605

Asn Thr Phe Pro Lys Arg Lys Lys Gly Glu Lys Arg Ala Ser Ser Pro
610 615 620

Phe Arg Arg Val Arg Glu Glu Glu Ile Glu Val Asp Ser Arg Val Ala
625 630 635 640

Asp Asn Ser Phe Asp Ala Lys Arg Gly Ala Ala Gly Asp Trp Gly Glu
645 650 655

Arg Ala Asn Gln Val Leu Lys Phe Thr Lys Gly Lys Ser Phe Arg His
660 665 670

Glu Lys Thr Lys Lys Lys Arg Gly Ser Tyr Arg Gly Gly Ser Ile Ser
675 680 685

Val Gln Val Asn Ser Ile Lys Phe Asp Ser Glu
690 695

<210> 33
<211> 4538
<212> DNA
<213> human

<220>
<221> CDS
<222> (26)..(4012)

<400> 33
tcgtgttttcg gtgagtggtgg cggag atg gag agc cgg gat ccc gcc cag ccg 52
Met Glu Ser Arg Asp Pro Ala Gln Pro
1 5

atg tcg cct gga gaa gcg acg cag agt ggc gcc cgg cct gcc gac cgc 100
Met Ser Pro Gly Glu Ala Thr Gln Ser Gly Ala Arg Pro Ala Asp Arg
10 15 20 25

tat ggc cta ttg aag cac agt cgc gag ttc ttg gac ttc ttc tgg gac 148
Tyr Gly Leu Leu Lys His Ser Arg Glu Phe Leu Asp Phe Phe Trp Asp
30 35 40

att gcg aag cct gag cag gag acg cga ctt gcg gcc acg gag aag ctg 196
Ile Ala Lys Pro Glu Gln Glu Thr Arg Leu Ala Ala Thr Glu Lys Leu
45 50 55

ctg gag tat ctg cgt ggc agg ccg aag ggg tcc gag atg aaa tat gcc 244
Leu Glu Tyr Leu Arg Gly Arg Pro Lys Gly Ser Glu Met Lys Tyr Ala
60 65 70

ctg aag cgt cta atc acg gga ctc ggg gtc ggg cga gaa aca gcc cgg 292
Leu Lys Arg Leu Ile Thr Gly Leu Gly Val Gly Arg Glu Thr Ala Arg
75 80 85

ccc tgc tac agt ttg gcc ctg gca cag ctg tta cag tct ttt gaa gac 340
Pro Cys Tyr Ser Leu Ala Leu Ala Gln Leu Leu Gln Ser Phe Glu Asp
90 95 100 105

ctc ccc ttg tgc agc atc ctg cag cag ata caa gaa aaa tat gac ctg 388
Leu Pro Leu Cys Ser Ile Leu Gln Gln Ile Gln Glu Lys Tyr Asp Leu
110 115 120

cat cag gtg aag aag gca atg ctg aga cct gct ctc ttt gca aac ctg 436
His Gln Val Lys Lys Ala Met Leu Arg Pro Ala Leu Phe Ala Asn Leu
125 130 135

ttt gga gtg ctc gcc ctc ttt cag tca ggt cgg ctg gtg aag gac cag 484
Phe Gly Val Leu Ala Leu Phe Gln Ser Gly Arg Leu Val Lys Asp Gln
140 145 150

gag gca ctg atg aag tcg gtg aag ctg ctg cag gcc ctg gcc cag tac	532
Glu Ala Leu Met Lys Ser Val Lys Leu Leu Gln Ala Leu Ala Gln Tyr	
155 160 165	
caa aac cac ttg cag gag cag ccc cgg aag gcc ctg gtg gac atc ctc	580
Gln Asn His Leu Gln Glu Gln Pro Arg Lys Ala Leu Val Asp Ile Leu	
170 175 180 185	
tcc gag gtc tcg aag gcc aca ttg cag gag atc ctg ccg gag gtc ctc	628
Ser Glu Val Ser Lys Ala Thr Leu Gln Glu Ile Leu Pro Glu Val Leu	
190 195 200	
aaa gcc gac ttg aat ata ata ctc agc tcc cct gaa cag cta gag ctc	676
Lys Ala Asp Leu Asn Ile Ile Leu Ser Ser Pro Glu Gln Leu Glu Leu	
205 210 215	
ttc ctc ctg gcc cag cag aag gtg ccc tcc aag ctc aag aag ctg gtg	724
Phe Leu Leu Ala Gln Gln Lys Val Pro Ser Lys Leu Lys Lys Leu Val	
220 225 230	
gga tcc gtg aac cta ttc tca gat gag aat gtc ccc agg ctg gtg aat	772
Gly Ser Val Asn Leu Phe Ser Asp Glu Asn Val Pro Arg Leu Val Asn	
235 240 245	
gtg ctg aag atg gcc gcc tcc tct gtg aag aag gac cgc aag ctg ccc	820
Val Leu Lys Met Ala Ala Ser Ser Val Lys Lys Asp Arg Lys Leu Pro	
250 255 260 265	
gcc att gct ctg gac ctg ctc cgc ctg gcg ctc aag gaa gac aag ttc	868
Ala Ile Ala Leu Asp Leu Leu Arg Leu Ala Leu Lys Glu Asp Lys Phe	
270 275 280	
cca cgg ttc tgg aag gag gtg gtg gaa caa ggg ctg ctg aag atg cag	916
Pro Arg Phe Trp Lys Glu Val Val Glu Gln Gly Leu Leu Lys Met Gln	
285 290 295	
ttc tgg cca gcc agc tac ctg tgt ttc cac ctg ctg ggc gcg gcc ctg	964
Phe Trp Pro Ala Ser Tyr Leu Cys Phe His Leu Leu Gly Ala Ala Leu	
300 305 310	
ccc ctg ctg acc aag gag cag ctg cac ctg gtg atg cag gga gac gtg	1012
Pro Leu Leu Thr Lys Glu Gln Leu His Leu Val Met Gln Gly Asp Val	
315 320 325	
atc cgc cat tac ggg gag cac gtg tgc act gct aag ctc cca aag cag	1060
Ile Arg His Tyr Gly Glu His Val Cys Thr Ala Lys Leu Pro Lys Gln	
330 335 340 345	
ttc aag ttt gcc cca gag atg gac gat tac gtg ggc acc ttc cta gag	1108
Phe Lys Phe Ala Pro Glu Met Asp Asp Tyr Val Gly Thr Phe Leu Glu	
350 355 360	
ggg tgc cag gat gac cct gag cgg cag ctg gcc gtg cta gtg gcc ttc	1156
Gly Cys Gln Asp Pro Glu Arg Gln Leu Ala Val Leu Val Ala Phe	
365 370 375	
tca tct gtc acc aac caa ggc ctc cct gtc acg cct act ttc tgg cgg	1204
Ser Ser Val Thr Asn Gln Gly Leu Pro Val Thr Pro Thr Phe Trp Arg	
380 385 390	

gtc	gtg	cgg	ttc	ctg	agc	cct	ccg	gcc	ctg	cag	ggc	tat	gtg	gcc	tgg	1252
Val	Val	Arg	Phe	Leu	Ser	Pro	Pro	Ala	Leu	Gln	Gly	Tyr	Val	Ala	Trp	
395						400					405					
ctg	cgg	gcc	atg	ttt	ctc	cag	cca	gac	ctg	gac	tcc	ttg	gtt	gac	ttc	1300
Leu	Arg	Ala	Met	Phe	Leu	Gln	Pro	Asp	Leu	Asp	Ser	Leu	Val	Asp	Phe	
410					415					420					425	
agc	acc	aac	aac	cag	aag	aaa	gcc	cag	gat	tca	tcg	ctc	cac	atg	cct	1348
Ser	Thr	Asn	Asn	Gln	Lys	Lys	Ala	Gln	Asp	Ser	Ser	Leu	His	Met	Pro	
				430					435					440		
gag	cga	gct	gtg	ttc	cgg	ctg	agg	aaa	tgg	atc	atc	ttt	cga	ttg	gtg	1396
Glu	Arg	Ala	Val	Phe	Arg	Leu	Arg	Lys	Trp	Ile	Ile	Phe	Arg	Leu	Val	
			445					450					455			
agc	att	gtg	gac	agc	ctg	cac	ctg	gag	atg	gag	gag	gcc	ttg	act	gag	1444
Ser	Ile	Val	Asp	Ser	Leu	His	Leu	Glu	Met	Glu	Glu	Ala	Leu	Thr	Glu	
		460					465					470				
cag	gtg	gcc	agg	ttt	tgt	ttg	ttc	cac	tcg	ttc	ttt	gtc	aca	aag	aag	1492
Gln	Val	Ala	Arg	Phe	Cys	Leu	Phe	His	Ser	Phe	Phe	Val	Thr	Lys	Lys	
	475					480					485					
ccc	aca	tcc	cag	atc	cct	gag	aca	aag	cac	ccg	ttc	tcc	ttc	cct	ttg	1540
Pro	Thr	Ser	Gln	Ile	Pro	Glu	Thr	Lys	His	Pro	Phe	Ser	Phe	Pro	Leu	
490					495					500					505	
gaa	aac	cag	gcc	cga	gag	gct	gtc	agc	agt	gcc	ttc	ttc	agt	ctg	ttg	1588
Glu	Asn	Gln	Ala	Arg	Glu	Ala	Val	Ser	Ser	Ala	Phe	Phe	Ser	Leu	Leu	
				510					515					520		
cag	acc	ctc	agc	acg	cag	ttc	aag	cag	gca	ccg	ggc	cag	acc	cag	ggt	1636
Gln	Thr	Leu	Ser	Thr	Gln	Phe	Lys	Gln	Ala	Pro	Gly	Gln	Thr	Gln	Gly	
			525					530					535			
ggg	cag	ccc	tgg	acc	tac	cac	ctg	gtg	caa	ttc	gca	gac	ctc	ctg	ttg	1684
Gly	Gln	Pro	Trp	Thr	Tyr	His	Leu	Val	Gln	Phe	Ala	Asp	Leu	Leu	Leu	
		540					545					550				
aat	cac	agc	cac	aac	gtg	acc	acc	gtg	aca	ccc	ttc	act	gcg	cag	cag	1732
Asn	His	Ser	His	Asn	Val	Thr	Thr	Val	Thr	Pro	Phe	Thr	Ala	Gln	Gln	
	555					560					565					
cac	cag	gcc	tgg	gac	cgg	atg	ctg	cag	act	ctg	aag	gag	ctg	gag	gcc	1780
His	Gln	Ala	Trp	Asp	Arg	Met	Leu	Gln	Thr	Leu	Lys	Glu	Leu	Glu	Ala	
570					575					580					585	
cac	tcc	gca	gag	gcc	agg	gct	gct	gcc	ttc	cag	cac	ctt	ctg	ctc	ttc	1828
His	Ser	Ala	Glu	Ala	Arg	Ala	Ala	Ala	Phe	Gln	His	Leu	Leu	Leu	Phe	
				590					595					600		
gtg	ggc	atc	cac	ctc	ctc	aag	tcc	cct	gca	gag	agc	tgt	gac	ctg	ctg	1876
Val	Gly	Ile	His	Leu	Leu	Lys	Ser	Pro	Ala	Glu	Ser	Cys	Asp	Leu	Leu	
			605					610					615			
ggt	gac	atc	cag	acc	tgc	atc	agg	aaa	agt	ctg	gga	gag	aag	ccc	cgc	1924
Gly	Asp	Ile	Gln	Thr	Cys	Ile	Arg	Lys	Ser	Leu	Gly	Glu	Lys	Pro	Arg	
		620					625					630				

cgg agc cgc acc aag acc atc gac ccc cag gaa ccc ccg tgg gta gag	1972
Arg Ser Arg Thr Lys Thr Ile Asp Pro Gln Glu Pro Trp Val Glu	
635 640 645	
gtg ctg gtg gag atc ttg ctg gcc ctg ttg gcc cag ccc agc cac ctc	2020
Val Leu Val Glu Ile Leu Leu Ala Leu Leu Ala Gln Pro Ser His Leu	
650 655 660 665	
atg cgc cag gtg gcc cgg agc gtg ttt ggc cac atc tgc tcc cac ctg	2068
Met Arg Gln Val Ala Arg Ser Val Phe Gly His Ile Cys Ser His Leu	
670 675 680	
acc ccg cgt gcc ctg cag cta att ctg gat gtg ctg aac ccc gag acc	2116
Thr Pro Arg Ala Leu Gln Leu Ile Leu Asp Val Leu Asn Pro Glu Thr	
685 690 695	
agt gag gat gag aat gac cgt gtg gtg gtg acg gac gat tct gat gag	2164
Ser Glu Asp Glu Asn Asp Arg Val Val Val Thr Asp Asp Ser Asp Glu	
700 705 710	
cgg cgg ctg aag ggt gca gag gac aag agc gag gaa ggt gag gac aac	2212
Arg Arg Leu Lys Gly Ala Glu Asp Lys Ser Glu Glu Gly Glu Asp Asn	
715 720 725	
aga agc tca gag agt gaa gag gag agc gag ggg gag gag agc gag gag	2260
Arg Ser Ser Glu Ser Glu Glu Glu Ser Glu Gly Glu Glu Ser Glu Glu	
730 735 740 745	
gag gag cgc gac ggg gac gtg gat cag ggc ttc cgg gaa cag ctg atg	2308
Glu Glu Arg Asp Gly Asp Val Asp Gln Gly Phe Arg Glu Gln Leu Met	
750 755 760	
acc gtg ctg cag gct ggg aag gcg ctg ggt gga gag gac agt gag aac	2356
Thr Val Leu Gln Ala Gly Lys Ala Leu Gly Gly Glu Asp Ser Glu Asn	
765 770 775	
gag gag gag ctg ggg gat gag gcc atg atg gcc ctg gac cag agc ctc	2404
Glu Glu Glu Leu Gly Asp Glu Ala Met Met Ala Leu Asp Gln Ser Leu	
780 785 790	
gcc agc ctc ttt gcc gag cag aag ctg cgt atc cag gcc cgg cga gac	2452
Ala Ser Leu Phe Ala Glu Gln Lys Leu Arg Ile Gln Ala Arg Arg Asp	
795 800 805	
gag aag aac aag ctg cag aag gag aag gct ctg cgg cgc gac ttc cag	2500
Glu Lys Asn Lys Leu Gln Lys Glu Lys Ala Leu Arg Arg Asp Phe Gln	
810 815 820 825	
atc cgg gtg ctg gac ctg gtg gag gtg cta gtg acc aag cag ccc gag	2548
Ile Arg Val Leu Asp Leu Val Glu Val Leu Val Thr Lys Gln Pro Glu	
830 835 840	
aat gcc ctg gtc ctg gag ctg ctg gag ccg ctg ctg agc atc atc cgg	2596
Asn Ala Leu Val Leu Glu Leu Leu Glu Pro Leu Leu Ser Ile Ile Arg	
845 850 855	
cgc agc ctg cgc agc agc agc tcc aaa cag gag cag gac ctt ctg cac	2644
Arg Ser Leu Arg Ser Ser Ser Ser Lys Gln Glu Gln Asp Leu Leu His	
860 865 870	

aag acg gcg cgc atc ttc acg cat cac ctg tgc cgt gcc cgg cgc tac	2692
Lys Thr Ala Arg Ile Phe Thr His His Leu Cys Arg Ala Arg Arg Tyr	
875 880 885	
tgc cac gac ttg ggt gag cgc gca ggg gcc ctg cac gcc cag gtg gag	2740
Cys His Asp Leu Gly Glu Arg Ala Gly Ala Leu His Ala Gln Val Glu	
890 895 900 905	
cgg ttg gtg cag cag gct ggc cgc cag ccc gac tcc ccc acc gcc ctc	2788
Arg Leu Val Gln Gln Ala Gly Arg Gln Pro Asp Ser Pro Thr Ala Leu	
910 915 920	
tac cac ttc aac gcc tct ctc tac ctg ctc cgg gtc ttg aag ggc aac	2836
Tyr His Phe Asn Ala Ser Leu Tyr Leu Leu Arg Val Leu Lys Gly Asn	
925 930 935	
act gct gag ggc tgc gtg cat gag aca cag gag aag cag aaa gct ggc	2884
Thr Ala Glu Gly Cys Val His Glu Thr Gln Glu Lys Gln Lys Ala Gly	
940 945 950	
act gac ccc agc cac atg ccc acg ggc ccg cag gct gcc agc tgc ttg	2932
Thr Asp Pro Ser His Met Pro Thr Gly Pro Gln Ala Ala Ser Cys Leu	
955 960 965	
gac ttg aac ctg gtg acc cgg gtg tac tcg aca gca ctg agc tcc ttc	2980
Asp Leu Asn Leu Val Thr Arg Val Tyr Ser Thr Ala Leu Ser Ser Phe	
970 975 980 985	
ctg acc aag cgc aac agc ccc ctc aca gtt ccc atg ttc ctc agc ctc	3028
Leu Thr Lys Arg Asn Ser Pro Leu Thr Val Pro Met Phe Leu Ser Leu	
990 995 1000	
ttc tcc cgg cac ccg gtg ctc tgt cag agc ctg ctc ccc atc ctg	3073
Phe Ser Arg His Pro Val Leu Cys Gln Ser Leu Leu Pro Ile Leu	
1005 1010 1015	
gtc cag cat atc acg ggc ccg gtg cgg ccc cgt cat cag gcc tgc	3118
Val Gln His Ile Thr Gly Pro Val Arg Pro Arg His Gln Ala Cys	
1020 1025 1030	
ctg ctg ctc cag aag acc ctg tcc atg cgg gag gtg agg tcg tgc	3163
Leu Leu Leu Gln Lys Thr Leu Ser Met Arg Glu Val Arg Ser Cys	
1035 1040 1045	
ttt gag gac ccc gag tgg aag cag ctg atg ggc cag gtc cta gca	3208
Phe Glu Asp Pro Glu Trp Lys Gln Leu Met Gly Gln Val Leu Ala	
1050 1055 1060	
aag gtc acc gag aac ttg cgc gtg ctg ggg gag gcg cag acc aag	3253
Lys Val Thr Glu Asn Leu Arg Val Leu Gly Glu Ala Gln Thr Lys	
1065 1070 1075	
gcg cag cat cag cag gca ctg tcc tcc ctg gag ctg ctc aac gtt	3298
Ala Gln His Gln Gln Ala Leu Ser Ser Leu Glu Leu Leu Asn Val	
1080 1085 1090	
ctc ttc agg acc tgc aaa cat gag aag ctg acc ttg gac ctg acg	3343
Leu Phe Arg Thr Cys Lys His Glu Lys Leu Thr Leu Asp Leu Thr	
1095 1100 1105	

gtg ctc ctg ggt	gtg ctg cag ggg	caa cag cag agc	cta cag cag	3388
Val Leu Leu Gly	Val Leu Gln Gly	Gln Gln Ser Leu	Gln Gln	
1110	1115	1120		
ggg gca cac tcc	acc ggc tcc agc	cgc ctg cac gac	ctc tac tgg	3433
Gly Ala His Ser	Thr Gly Ser Ser	Arg Leu His Asp	Leu Tyr Trp	
1125	1130	1135		
cag gcc atg aaa	acc ctg gga gtc	cag cgc ccc aag	ttg gag aag	3478
Gln Ala Met Lys	Thr Leu Gly Val	Gln Arg Pro Lys	Leu Glu Lys	
1140	1145	1150		
aag gat gcc aag	gag atc ccc agt	gcc acc cag agc	ccc atc agt	3523
Lys Asp Ala Lys	Glu Ile Pro Ser	Ala Thr Gln Ser	Pro Ile Ser	
1155	1160	1165		
aag aag cgg aag	aaa aag gga ttc	ttg cca gag acg	aag aag cgc	3568
Lys Lys Arg Lys	Lys Lys Gly Phe	Leu Pro Glu Thr	Lys Lys Arg	
1170	1175	1180		
aag aaa cgc aag	tca gag gat ggc	acg cca gcg gag	gat ggc aca	3613
Lys Lys Arg Lys	Ser Glu Asp Gly	Thr Pro Ala Glu	Asp Gly Thr	
1185	1190	1195		
cct gca gcc acc	ggc ggg agc cag	ccc ccc agc atg	ggc agg aag	3658
Pro Ala Ala Thr	Gly Gly Ser Gln	Pro Pro Ser Met	Gly Arg Lys	
1200	1205	1210		
aag agg aac agg	aca aag gct aag	gtc cca gcc cag	gca aac ggg	3703
Lys Arg Asn Arg	Thr Lys Ala Lys	Val Pro Ala Gln	Ala Asn Gly	
1215	1220	1225		
acg cca acc acc	aag agt cca gcc	cct ggc gcc ccc	acc cgg agc	3748
Thr Pro Thr Thr	Lys Ser Pro Ala	Pro Gly Ala Pro	Thr Arg Ser	
1230	1235	1240		
ccc agc acc cct	gcc aaa tcc cca	aaa ctg cag aag	aaa aac cag	3793
Pro Ser Thr Pro	Ala Lys Ser Pro	Lys Leu Gln Lys	Lys Asn Gln	
1245	1250	1255		
aag ccg tcc cag	gtg aat gga gct	ccc ggg tcc ccc	acg gaa cct	3838
Lys Pro Ser Gln	Val Asn Gly Ala	Pro Gly Ser Pro	Thr Glu Pro	
1260	1265	1270		
gca ggc caa aag	cag cat cag aag	gct ctt ccc aaa	aag ggg gtc	3883
Ala Gly Gln Lys	Gln His Gln Lys	Ala Leu Pro Lys	Lys Gly Val	
1275	1280	1285		
ttg ggc aaa tca	cca ctg tcc gcg	ctg gca cgg aaa	aag gca agg	3928
Leu Gly Lys Ser	Pro Leu Ser Ala	Leu Ala Arg Lys	Lys Ala Arg	
1290	1295	1300		
ctg tct ttg gtc	atc agg agt ccc	agc ctg ctt cag	agt ggg gcc	3973
Leu Ser Leu Val	Ile Arg Ser Pro	Ser Leu Leu Gln	Ser Gly Ala	
1305	1310	1315		
aag aag aaa gca	cag gtg agg aag	gca ggg aag ccc	tga gcacaggtac	4022
Lys Lys Lys Ala	Gln Val Arg Lys	Ala Gly Lys Pro		
1320	1325			

```

gggccccccct cagccccctgc ctccatctgc ctgagacgcc tattttttttt tttttaaaac 4082
catgatttta atacgcaagc tgtttctaag gcgctgccac tggggagggt ggctgttgcc 4142
gcctgcccgg gcacacctgct ctggcaagca cagcctgagc cattcctgcg ggggtcccag 4202
ggtgcagaga cctccccacc ccagttctg ggctgggatc ctggctccag ggccatgtcc 4262
agggctcttg tgtttgctg ggttggtgca tgttgatgtg ctggctgcag gcaggtgtga 4322
ccatctctcg tgcctgccac ctctttgccc ccaggctttt ttgctgtgag ggagccacca 4382
gggggtgatt taaatagggt tattttcttca ttacaagag gaatatattt ggcttctctc 4442
ttaagactct gagattcaca atcagcagct ctaaaaaata aaggagcagt ttggcttccg 4502
gaaggaagag gaggctaaaa aaaaaaaaaa aaaaaa 4538

```

```

<210> 34
<211> 1328
<212> PRT
<213> human

```

```

<400> 34

```

```

Met Glu Ser Arg Asp Pro Ala Gln Pro Met Ser Pro Gly Glu Ala Thr
1          5          10          15

```

```

Gln Ser Gly Ala Arg Pro Ala Asp Arg Tyr Gly Leu Leu Lys His Ser
          20          25          30

```

```

Arg Glu Phe Leu Asp Phe Phe Trp Asp Ile Ala Lys Pro Glu Gln Glu
          35          40          45

```

```

Thr Arg Leu Ala Ala Thr Glu Lys Leu Leu Glu Tyr Leu Arg Gly Arg
          50          55          60

```

```

Pro Lys Gly Ser Glu Met Lys Tyr Ala Leu Lys Arg Leu Ile Thr Gly
          65          70          75          80

```

```

Leu Gly Val Gly Arg Glu Thr Ala Arg Pro Cys Tyr Ser Leu Ala Leu
          85          90          95

```

```

Ala Gln Leu Leu Gln Ser Phe Glu Asp Leu Pro Leu Cys Ser Ile Leu
          100          105          110

```

```

Gln Gln Ile Gln Glu Lys Tyr Asp Leu His Gln Val Lys Lys Ala Met
          115          120          125

```

```

Leu Arg Pro Ala Leu Phe Ala Asn Leu Phe Gly Val Leu Ala Leu Phe

```

130	135	140
Gln Ser Gly Arg Leu Val Lys Asp Gln Glu Ala Leu Met Lys Ser Val 145 150 155 160		
Lys Leu Leu Gln Ala Leu Ala Gln Tyr Gln Asn His Leu Gln Glu Gln 165 170 175		
Pro Arg Lys Ala Leu Val Asp Ile Leu Ser Glu Val Ser Lys Ala Thr 180 185 190		
Leu Gln Glu Ile Leu Pro Glu Val Leu Lys Ala Asp Leu Asn Ile Ile 195 200 205		
Leu Ser Ser Pro Glu Gln Leu Glu Leu Phe Leu Leu Ala Gln Gln Lys 210 215 220		
Val Pro Ser Lys Leu Lys Lys Leu Val Gly Ser Val Asn Leu Phe Ser 225 230 235 240		
Asp Glu Asn Val Pro Arg Leu Val Asn Val Leu Lys Met Ala Ala Ser 245 250 255		
Ser Val Lys Lys Asp Arg Lys Leu Pro Ala Ile Ala Leu Asp Leu Leu 260 265 270		
Arg Leu Ala Leu Lys Glu Asp Lys Phe Pro Arg Phe Trp Lys Glu Val 275 280 285		
Val Glu Gln Gly Leu Leu Lys Met Gln Phe Trp Pro Ala Ser Tyr Leu 290 295 300		
Cys Phe His Leu Leu Gly Ala Ala Leu Pro Leu Leu Thr Lys Glu Gln 305 310 315 320		
Leu His Leu Val Met Gln Gly Asp Val Ile Arg His Tyr Gly Glu His 325 330 335		
Val Cys Thr Ala Lys Leu Pro Lys Gln Phe Lys Phe Ala Pro Glu Met 340 345 350		
Asp Asp Tyr Val Gly Thr Phe Leu Glu Gly Cys Gln Asp Asp Pro Glu 355 360 365		
Arg Gln Leu Ala Val Leu Val Ala Phe Ser Ser Val Thr Asn Gln Gly		

370	375	380
Leu Pro Val Thr Pro Thr Phe Trp Arg Val Val Arg Phe Leu Ser Pro 385 390 395 400		
Pro Ala Leu Gln Gly Tyr Val Ala Trp Leu Arg Ala Met Phe Leu Gln 405 410 415		
Pro Asp Leu Asp Ser Leu Val Asp Phe Ser Thr Asn Asn Gln Lys Lys 420 425 430		
Ala Gln Asp Ser Ser Leu His Met Pro Glu Arg Ala Val Phe Arg Leu 435 440 445		
Arg Lys Trp Ile Ile Phe Arg Leu Val Ser Ile Val Asp Ser Leu His 450 455 460		
Leu Glu Met Glu Glu Ala Leu Thr Glu Gln Val Ala Arg Phe Cys Leu 465 470 475 480		
Phe His Ser Phe Phe Val Thr Lys Lys Pro Thr Ser Gln Ile Pro Glu 485 490 495		
Thr Lys His Pro Phe Ser Phe Pro Leu Glu Asn Gln Ala Arg Glu Ala 500 505 510		
Val Ser Ser Ala Phe Phe Ser Leu Leu Gln Thr Leu Ser Thr Gln Phe 515 520 525		
Lys Gln Ala Pro Gly Gln Thr Gln Gly Gly Gln Pro Trp Thr Tyr His 530 535 540		
Leu Val Gln Phe Ala Asp Leu Leu Leu Asn His Ser His Asn Val Thr 545 550 555 560		
Thr Val Thr Pro Phe Thr Ala Gln Gln His Gln Ala Trp Asp Arg Met 565 570 575		
Leu Gln Thr Leu Lys Glu Leu Glu Ala His Ser Ala Glu Ala Arg Ala 580 585 590		
Ala Ala Phe Gln His Leu Leu Leu Phe Val Gly Ile His Leu Leu Lys 595 600 605		
Ser Pro Ala Glu Ser Cys Asp Leu Leu Gly Asp Ile Gln Thr Cys Ile		

610	615	620
Arg Lys Ser Leu Gly Glu Lys Pro Arg Arg Ser Arg Thr Lys Thr Ile 625 630 635 640		
Asp Pro Gln Glu Pro Pro Trp Val Glu Val Leu Val Glu Ile Leu Leu 645 650 655		
Ala Leu Leu Ala Gln Pro Ser His Leu Met Arg Gln Val Ala Arg Ser 660 665 670		
Val Phe Gly His Ile Cys Ser His Leu Thr Pro Arg Ala Leu Gln Leu 675 680 685		
Ile Leu Asp Val Leu Asn Pro Glu Thr Ser Glu Asp Glu Asn Asp Arg 690 695 700		
Val Val Val Thr Asp Asp Ser Asp Glu Arg Arg Leu Lys Gly Ala Glu 705 710 715 720		
Asp Lys Ser Glu Glu Gly Glu Asp Asn Arg Ser Ser Glu Ser Glu Glu 725 730 735		
Glu Ser Glu Gly Glu Glu Ser Glu Glu Glu Glu Arg Asp Gly Asp Val 740 745 750		
Asp Gln Gly Phe Arg Glu Gln Leu Met Thr Val Leu Gln Ala Gly Lys 755 760 765		
Ala Leu Gly Gly Glu Asp Ser Glu Asn Glu Glu Glu Leu Gly Asp Glu 770 775 780		
Ala Met Met Ala Leu Asp Gln Ser Leu Ala Ser Leu Phe Ala Glu Gln 785 790 795 800		
Lys Leu Arg Ile Gln Ala Arg Arg Asp Glu Lys Asn Lys Leu Gln Lys 805 810 815		
Glu Lys Ala Leu Arg Arg Asp Phe Gln Ile Arg Val Leu Asp Leu Val 820 825 830		
Glu Val Leu Val Thr Lys Gln Pro Glu Asn Ala Leu Val Leu Glu Leu 835 840 845		
Leu Glu Pro Leu Leu Ser Ile Ile Arg Arg Ser Leu Arg Ser Ser Ser		

850		855		860											
Ser 865	Lys	Gln	Glu	Gln	Asp	Leu	Leu	His	Lys	Thr	Ala	Arg	Ile	Phe	Thr 880
					870					875					
His	His	Leu	Cys	Arg	Ala	Arg	Arg	Tyr	Cys	His	Asp	Leu	Gly	Glu	Arg 895
				885					890						
Ala	Gly	Ala	Leu	His	Ala	Gln	Val	Glu	Arg	Leu	Val	Gln	Gln	Ala	Gly
			900					905					910		
Arg	Gln	Pro	Asp	Ser	Pro	Thr	Ala	Leu	Tyr	His	Phe	Asn	Ala	Ser	Leu
		915					920					925			
Tyr	Leu	Leu	Arg	Val	Leu	Lys	Gly	Asn	Thr	Ala	Glu	Gly	Cys	Val	His
930						935					940				
Glu	Thr	Gln	Glu	Lys	Gln	Lys	Ala	Gly	Thr	Asp	Pro	Ser	His	Met	Pro
945					950					955					960
Thr	Gly	Pro	Gln	Ala	Ala	Ser	Cys	Leu	Asp	Leu	Asn	Leu	Val	Thr	Arg
				965					970					975	
Val	Tyr	Ser	Thr	Ala	Leu	Ser	Ser	Phe	Leu	Thr	Lys	Arg	Asn	Ser	Pro
			980					985					990		
Leu	Thr	Val	Pro	Met	Phe	Leu	Ser	Leu	Phe	Ser	Arg	His	Pro	Val	Leu
		995					1000					1005			
Cys	Gln	Ser	Leu	Leu	Pro	Ile	Leu	Val	Gln	His	Ile	Thr	Gly	Pro	
1010						1015					1020				
Val	Arg	Pro	Arg	His	Gln	Ala	Cys	Leu	Leu	Leu	Gln	Lys	Thr	Leu	
1025						1030					1035				
Ser	Met	Arg	Glu	Val	Arg	Ser	Cys	Phe	Glu	Asp	Pro	Glu	Trp	Lys	
1040						1045					1050				
Gln	Leu	Met	Gly	Gln	Val	Leu	Ala	Lys	Val	Thr	Glu	Asn	Leu	Arg	
1055						1060					1065				
Val	Leu	Gly	Glu	Ala	Gln	Thr	Lys	Ala	Gln	His	Gln	Gln	Ala	Leu	
1070						1075					1080				
Ser	Ser	Leu	Glu	Leu	Leu	Asn	Val	Leu	Phe	Arg	Thr	Cys	Lys	His	

1085		1090		1095
Glu Lys Leu Thr Leu Asp Leu Thr Val Leu Leu Gly Val Leu Gln				
1100		1105		1110
Gly Gln Gln Gln Ser Leu Gln Gln Gly Ala His Ser Thr Gly Ser				
1115		1120		1125
Ser Arg Leu His Asp Leu Tyr Trp Gln Ala Met Lys Thr Leu Gly				
1130		1135		1140
Val Gln Arg Pro Lys Leu Glu Lys Lys Asp Ala Lys Glu Ile Pro				
1145		1150		1155
Ser Ala Thr Gln Ser Pro Ile Ser Lys Lys Arg Lys Lys Lys Gly				
1160		1165		1170
Phe Leu Pro Glu Thr Lys Lys Arg Lys Lys Arg Lys Ser Glu Asp				
1175		1180		1185
Gly Thr Pro Ala Glu Asp Gly Thr Pro Ala Ala Thr Gly Gly Ser				
1190		1195		1200
Gln Pro Pro Ser Met Gly Arg Lys Lys Arg Asn Arg Thr Lys Ala				
1205		1210		1215
Lys Val Pro Ala Gln Ala Asn Gly Thr Pro Thr Thr Lys Ser Pro				
1220		1225		1230
Ala Pro Gly Ala Pro Thr Arg Ser Pro Ser Thr Pro Ala Lys Ser				
1235		1240		1245
Pro Lys Leu Gln Lys Lys Asn Gln Lys Pro Ser Gln Val Asn Gly				
1250		1255		1260
Ala Pro Gly Ser Pro Thr Glu Pro Ala Gly Gln Lys Gln His Gln				
1265		1270		1275
Lys Ala Leu Pro Lys Lys Gly Val Leu Gly Lys Ser Pro Leu Ser				
1280		1285		1290
Ala Leu Ala Arg Lys Lys Ala Arg Leu Ser Leu Val Ile Arg Ser				
1295		1300		1305
Pro Ser Leu Leu Gln Ser Gly Ala Lys Lys Lys Ala Gln Val Arg				

1310

1315

1320

Lys Ala Gly Lys Pro
1325

<210> 35
<211> 2427
<212> DNA
<213> human

<220>
<221> CDS
<222> (86)..(1681)

<400> 35
gggatttggtt attgcgaatg atgtggacaa caagcgctgc tacctgctcg tccatcaagc 60

caagaggctg agcagcccct gcatc atg gtg gtc aac cat gat gcc tcc agc 112
Met Val Val Asn His Asp Ala Ser Ser
1 5

ata ccc agg ctc cag ata gat gtg gac ggc agg aaa gag atc ctc ttc 160
Ile Pro Arg Leu Gln Ile Asp Val Asp Gly Arg Lys Glu Ile Leu Phe
10 15 20 25

tat gat cga att tta tgt gat gtc cct tgc agt gga gac ggc act atg 208
Tyr Asp Arg Ile Leu Cys Asp Val Pro Cys Ser Gly Asp Gly Thr Met
30 35 40

aga aaa aac att gat gtt tgg aaa aag tgg acc acc tta aat agc ttg 256
Arg Lys Asn Ile Asp Val Trp Lys Lys Trp Thr Thr Leu Asn Ser Leu
45 50 55

cag cta cat ggc tta cag ctg cgg att gca aca cgc ggg gct gaa cag 304
Gln Leu His Gly Leu Gln Leu Arg Ile Ala Thr Arg Gly Ala Glu Gln
60 65 70

ctg gct gaa ggt gga agg gtg gtg tat tcc acg tgt tca cta aac cct 352
Leu Ala Glu Gly Gly Arg Val Val Tyr Ser Thr Cys Ser Leu Asn Pro
75 80 85

att gag gat gaa gca gtc ata gca tct tta ctg gaa aaa agt gaa ggt 400
Ile Glu Asp Glu Ala Val Ile Ala Ser Leu Leu Glu Lys Ser Glu Gly
90 95 100 105

gct ttg gag ctt gct gat gtg tct aat gaa ctg cca ggg ctg aag tgg 448
Ala Leu Glu Leu Ala Asp Val Ser Asn Glu Leu Pro Gly Leu Lys Trp
110 115 120

atg cct gga atc aca cag tgg aag gta atg acg aaa gat ggg cag tgg 496
Met Pro Gly Ile Thr Gln Trp Lys Val Met Thr Lys Asp Gly Gln Trp
125 130 135

ttt aca gac tgg gac gct gtt cct cac agc aga cac acc cag atc cga 544
Phe Thr Asp Trp Asp Ala Val Pro His Ser Arg His Thr Gln Ile Arg
140 145 150

cct acc atg ttc cct ccg aag gac cca gaa aag ctg cag gcc atg cac	592
Pro Thr Met Phe Pro Pro Lys Asp Pro Glu Lys Leu Gln Ala Met His	
155 160 165	
ctg gag cga tgc ctt agg ata tta ccc cat cat cag aat act gga ggg	640
Leu Glu Arg Cys Leu Arg Ile Leu Pro His His Gln Asn Thr Gly Gly	
170 175 180 185	
ttt ttt gtg gca gta ttg gtg aaa aaa tct tca atg ccg tgg aat aaa	688
Phe Phe Val Ala Val Leu Val Lys Lys Ser Ser Met Pro Trp Asn Lys	
190 195 200	
cgt cag cca aag ctt cag ggt aaa tct gca gag acc aga gaa agc aca	736
Arg Gln Pro Lys Leu Gln Gly Lys Ser Ala Glu Thr Arg Glu Ser Thr	
205 210 215	
cag ctg agc cct gca gat ctc aca gaa ggg aaa ccc aca gat ccc tct	784
Gln Leu Ser Pro Ala Asp Leu Thr Glu Gly Lys Pro Thr Asp Pro Ser	
220 225 230	
aag ctg gaa agt ccg tca ttc aca gga act ggt gac aca gaa ata gct	832
Lys Leu Glu Ser Pro Ser Phe Thr Gly Thr Gly Asp Thr Glu Ile Ala	
235 240 245	
cat gca act gag gat tta gag aat aat ggc agt aag aaa gat ggc gtg	880
His Ala Thr Glu Asp Leu Glu Asn Asn Gly Ser Lys Lys Asp Gly Val	
250 255 260 265	
tgt ggt cct cct cca tca aag aaa atg aag tta ttt gga ttt aaa gaa	928
Cys Gly Pro Pro Ser Lys Lys Met Lys Leu Phe Gly Phe Lys Glu	
270 275 280	
gat cca ttt gta ttt att cct gaa gat gac cca tta ttt cca cct att	976
Asp Pro Phe Val Phe Ile Pro Glu Asp Asp Pro Leu Phe Pro Pro Ile	
285 290 295	
gag aaa ttt tat gct ttg gat cct tca ttc cca agg atg aat ttg tta	1024
Glu Lys Phe Tyr Ala Leu Asp Pro Ser Phe Pro Arg Met Asn Leu Leu	
300 305 310	
act cgg act aca gaa ggg aag aaa agg cag ctc tac atg gtt tct aag	1072
Thr Arg Thr Thr Glu Gly Lys Lys Arg Gln Leu Tyr Met Val Ser Lys	
315 320 325	
gag ttg cgg aat gtg ctg ctg aat aac agt gag aag atg aag gtt att	1120
Glu Leu Arg Asn Val Leu Leu Asn Asn Ser Glu Lys Met Lys Val Ile	
330 335 340 345	
aac acg ggg atc aaa gtc tgg tgt aga aat aac agc ggt gaa gag ttt	1168
Asn Thr Gly Ile Lys Val Trp Cys Arg Asn Asn Ser Gly Glu Glu Phe	
350 355 360	
gac tgt gct ttc cgg ctg gca cag gag gga ata tat aca ttg tat cca	1216
Asp Cys Ala Phe Arg Leu Ala Gln Glu Gly Ile Tyr Thr Leu Tyr Pro	
365 370 375	
ttt att aac tca aga att att act gta tca atg gaa gat gtt aag ata	1264
Phe Ile Asn Ser Arg Ile Ile Thr Val Ser Met Glu Asp Val Lys Ile	
380 385 390	

ctg ttg acc cag gaa aat ccc ttt ttt aga aaa ctc agc agt gag acc	1312
Leu Leu Thr Gln Glu Asn Pro Phe Phe Arg Lys Leu Ser Ser Glu Thr	
395 400 405	
tac agt caa gca aag gac ctg gca aag gga agc atc gtg ctg aag tat	1360
Tyr Ser Gln Ala Lys Asp Leu Ala Lys Gly Ser Ile Val Leu Lys Tyr	
410 415 420 425	
gaa cca gat tct gcg aat cca gac gct cta cag tgt ccc atc gtc tta	1408
Glu Pro Asp Ser Ala Asn Pro Asp Ala Leu Gln Cys Pro Ile Val Leu	
430 435 440	
tgc gga tgg cgg gga aag gcc tcc att cga act ttt gtg ccc aag aat	1456
Cys Gly Trp Arg Gly Lys Ala Ser Ile Arg Thr Phe Val Pro Lys Asn	
445 450 455	
gaa cgg ctt cac tat ctc agg atg atg ggg ctg gag gta ttg gga gaa	1504
Glu Arg Leu His Tyr Leu Arg Met Met Gly Leu Glu Val Leu Gly Glu	
460 465 470	
aag aag aag gaa ggg gtt atc ctc aca aat gag agt gca gcc agc acc	1552
Lys Lys Lys Glu Gly Val Ile Leu Thr Asn Glu Ser Ala Ala Ser Thr	
475 480 485	
gga cag cca gac aat gac gtg act gag gga cag aga gca gga gag ccc	1600
Gly Gln Pro Asp Asn Asp Val Thr Glu Gly Gln Arg Ala Gly Glu Pro	
490 495 500 505	
aac agc cca gat gca gaa gag gcc aac agt cca gac gtg aca gca ggc	1648
Asn Ser Pro Asp Ala Glu Glu Ala Asn Ser Pro Asp Val Thr Ala Gly	
510 515 520	
tgt gac ccg gcg ggg gtc cat cca ccc cgg tga gcaggcccaa ggcagcgggg	1701
Cys Asp Pro Ala Gly Val His Pro Pro Arg	
525 530	
gccccacacc ctcacacgca aaactggcctt cttctgggtca ctggtgtctg aaaccaaatac	1761
cagagcagcc tgtggcctgt aaagcatata tttctagtga ctgcagactg gtgggatcat	1821
aggagccttc tgaatgacca ggactgcttt ctttggagct gatgaaaatg tactctttta	1881
gcgtgttaga aatcacttgt tttattttgt tttctttggc caagctgggt ctagtgtttc	1941
ttttgctggg aatagacttt caaaagttgt acttctatca agaaacaaaa ctgcccttgc	2001
agaaatttca ggtcttttgt taagcctgta ttggtcttaa ggtgcagtat tttttaaat	2061
attatttata gaaagaatct ataaattctt ggggaagtgt gttataagct ttaataatta	2121
cattgagctg cacctcagt gtgtgtcatt aacatgcagt ggggttaata tctgaggcct	2181
cagatgactt tgtgcctttt ggaataaagg gtaaaataaa ctctcccaga gtaagagctg	2241
tatcgtgaat tgtcatacta attattgagg gggacttatg tgctttttatt gaatggagt	2301
ctttacaatt tttattttta aatgggggttg ggatccttgg aatatttcaa taaaattgat	2361
aaaatataaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa	2421

aaaaaa

2427

<210> 36
<211> 531
<212> PRT
<213> human

<400> 36

Met Val Val Asn His Asp Ala Ser Ser Ile Pro Arg Leu Gln Ile Asp
1 5 10 15

Val Asp Gly Arg Lys Glu Ile Leu Phe Tyr Asp Arg Ile Leu Cys Asp
20 25 30

Val Pro Cys Ser Gly Asp Gly Thr Met Arg Lys Asn Ile Asp Val Trp
35 40 45

Lys Lys Trp Thr Thr Leu Asn Ser Leu Gln Leu His Gly Leu Gln Leu
50 55 60

Arg Ile Ala Thr Arg Gly Ala Glu Gln Leu Ala Glu Gly Gly Arg Val
65 70 75 80

Val Tyr Ser Thr Cys Ser Leu Asn Pro Ile Glu Asp Glu Ala Val Ile
85 90 95

Ala Ser Leu Leu Glu Lys Ser Glu Gly Ala Leu Glu Leu Ala Asp Val
100 105 110

Ser Asn Glu Leu Pro Gly Leu Lys Trp Met Pro Gly Ile Thr Gln Trp
115 120 125

Lys Val Met Thr Lys Asp Gly Gln Trp Phe Thr Asp Trp Asp Ala Val
130 135 140

Pro His Ser Arg His Thr Gln Ile Arg Pro Thr Met Phe Pro Pro Lys
145 150 155 160

Asp Pro Glu Lys Leu Gln Ala Met His Leu Glu Arg Cys Leu Arg Ile
165 170 175

Leu Pro His His Gln Asn Thr Gly Gly Phe Phe Val Ala Val Leu Val
180 185 190

Lys Lys Ser Ser Met Pro Trp Asn Lys Arg Gln Pro Lys Leu Gln Gly
195 200 205

Lys Ser Ala Glu Thr Arg Glu Ser Thr Gln Leu Ser Pro Ala Asp Leu
210 215 220

Thr Glu Gly Lys Pro Thr Asp Pro Ser Lys Leu Glu Ser Pro Ser Phe
225 230 235 240

Thr Gly Thr Gly Asp Thr Glu Ile Ala His Ala Thr Glu Asp Leu Glu
245 250 255

Asn Asn Gly Ser Lys Lys Asp Gly Val Cys Gly Pro Pro Pro Ser Lys
260 265 270

Lys Met Lys Leu Phe Gly Phe Lys Glu Asp Pro Phe Val Phe Ile Pro
275 280 285

Glu Asp Asp Pro Leu Phe Pro Pro Ile Glu Lys Phe Tyr Ala Leu Asp
290 295 300

Pro Ser Phe Pro Arg Met Asn Leu Leu Thr Arg Thr Thr Glu Gly Lys
305 310 315 320

Lys Arg Gln Leu Tyr Met Val Ser Lys Glu Leu Arg Asn Val Leu Leu
325 330 335

Asn Asn Ser Glu Lys Met Lys Val Ile Asn Thr Gly Ile Lys Val Trp
340 345 350

Cys Arg Asn Asn Ser Gly Glu Glu Phe Asp Cys Ala Phe Arg Leu Ala
355 360 365

Gln Glu Gly Ile Tyr Thr Leu Tyr Pro Phe Ile Asn Ser Arg Ile Ile
370 375 380

Thr Val Ser Met Glu Asp Val Lys Ile Leu Leu Thr Gln Glu Asn Pro
385 390 395 400

Phe Phe Arg Lys Leu Ser Ser Glu Thr Tyr Ser Gln Ala Lys Asp Leu
405 410 415

Ala Lys Gly Ser Ile Val Leu Lys Tyr Glu Pro Asp Ser Ala Asn Pro
420 425 430

Asp Ala Leu Gln Cys Pro Ile Val Leu Cys Gly Trp Arg Gly Lys Ala
435 440 445

Ser Ile Arg Thr Phe Val Pro Lys Asn Glu Arg Leu His Tyr Leu Arg
 450 455 460

Met Met Gly Leu Glu Val Leu Gly Glu Lys Lys Lys Glu Gly Val Ile
 465 470 475 480

Leu Thr Asn Glu Ser Ala Ala Ser Thr Gly Gln Pro Asp Asn Asp Val
 485 490 495

Thr Glu Gly Gln Arg Ala Gly Glu Pro Asn Ser Pro Asp Ala Glu Glu
 500 505 510

Ala Asn Ser Pro Asp Val Thr Ala Gly Cys Asp Pro Ala Gly Val His
 515 520 525

Pro Pro Arg
 530

<210> 37
 <211> 1792
 <212> DNA
 <213> human

<220>
 <221> CDS
 <222> (61)..(1281)

<400> 37
 cttgaggggga agaggctgac tgtacgttcc ttctactctg gcaccactct ccaggctgcc 60
 atg ggg ccc agc acc cct ctc ctc atc ttg ttc ctt ttg tca tgg tcg 108
 Met Gly Pro Ser Thr Pro Leu Leu Ile Leu Phe Leu Leu Ser Trp Ser
 1 5 10 15
 gga ccc ctc caa gga cag cag cac cac ctt gtg gag tac atg gaa cgc 156
 Gly Pro Leu Gln Gly Gln Gln His His Leu Val Glu Tyr Met Glu Arg
 20 25 30
 cga cta gct gct tta gag gaa cgg ctg gcc cag tgc cag gac cag agt 204
 Arg Leu Ala Ala Leu Glu Glu Arg Leu Ala Gln Cys Gln Asp Gln Ser
 35 40 45
 agt cgg cat gct gct gag ctg cgg gac ttc aag aac aag atg ctg cca 252
 Ser Arg His Ala Ala Glu Leu Arg Asp Phe Lys Asn Lys Met Leu Pro
 50 55 60
 ctg ctg gag gtg gca gag aag gag cgg gag gca ctc aga act gag gcc 300
 Leu Leu Glu Val Ala Glu Lys Glu Arg Glu Ala Leu Arg Thr Glu Ala
 65 70 75 80
 gac acc atc tcc ggg aga gtg gat cgt ctg gag cgg gag gta gac tat 348

Asp	Thr	Ile	Ser	Gly	Arg	Val	Asp	Arg	Leu	Glu	Arg	Glu	Val	Asp	Tyr		
				85					90					95			
ctg	gag	acc	cag	aac	cca	gct	ctg	ccc	tgt	gta	gag	ttt	gat	gag	aag	396	
Leu	Glu	Thr	Gln	Asn	Pro	Ala	Leu	Pro	Cys	Val	Glu	Phe	Asp	Glu	Lys		
			100					105					110				
gtg	act	gga	ggc	cct	ggg	acc	aaa	ggc	aag	gga	aga	agg	aat	gag	aag	444	
Val	Thr	Gly	Gly	Pro	Gly	Thr	Lys	Gly	Lys	Gly	Arg	Arg	Asn	Glu	Lys		
		115					120					125					
tac	gat	atg	gtg	aca	gac	tgt	ggc	tac	aca	atc	tct	caa	gtg	aga	tca	492	
Tyr	Asp	Met	Val	Thr	Asp	Cys	Gly	Tyr	Thr	Ile	Ser	Gln	Val	Arg	Ser		
	130					135					140						
atg	aag	att	ctg	aag	cga	ttt	ggg	ggc	cca	gct	ggg	cta	tgg	acc	aag	540	
Met	Lys	Ile	Leu	Lys	Arg	Phe	Gly	Gly	Pro	Ala	Gly	Leu	Trp	Thr	Lys		
145					150					155					160		
gat	cca	ctg	ggg	caa	aca	gag	aag	atc	tac	gtg	tta	gat	ggg	aca	cag	588	
Asp	Pro	Leu	Gly	Gln	Thr	Glu	Lys	Ile	Tyr	Val	Leu	Asp	Gly	Thr	Gln		
				165					170					175			
aat	gac	aca	gcc	ttt	gtc	ttc	cca	agg	ctg	cgt	gac	ttc	acc	ctt	gcc	636	
Asn	Asp	Thr	Ala	Phe	Val	Phe	Pro	Arg	Leu	Arg	Asp	Phe	Thr	Leu	Ala		
		180						185					190				
atg	gct	gcc	cgg	aaa	gct	tcc	cga	gtc	cgg	gtg	ccc	ttc	ccc	tgg	gta	684	
Met	Ala	Ala	Arg	Lys	Ala	Ser	Arg	Val	Arg	Val	Pro	Phe	Pro	Trp	Val		
		195					200					205					
ggc	aca	ggg	cag	ctg	gta	tat	ggg	ggc	ttt	ctt	tat	ttt	gct	cgg	agg	732	
Gly	Thr	Gly	Gln	Leu	Val	Tyr	Gly	Gly	Phe	Leu	Tyr	Phe	Ala	Arg	Arg		
	210					215					220						
cct	cct	gga	aga	cct	ggg	gga	ggg	ggg	gag	atg	gag	aac	act	ttg	cag	780	
Pro	Pro	Gly	Arg	Pro	Gly	Gly	Gly	Gly	Glu	Met	Glu	Asn	Thr	Leu	Gln		
225					230					235					240		
cta	atc	aaa	ttc	cac	ctg	gca	aac	cga	aca	gtg	gtg	gac	agc	tca	gta	828	
Leu	Ile	Lys	Phe	His	Leu	Ala	Asn	Arg	Thr	Val	Val	Asp	Ser	Ser	Val		
				245					250					255			
ttc	cca	gca	gag	ggg	ctg	atc	ccc	ccc	tac	ggc	ttg	aca	gca	gac	acc	876	
Phe	Pro	Ala	Glu	Gly	Leu	Ile	Pro	Pro	Tyr	Gly	Leu	Thr	Ala	Asp	Thr		
			260					265					270				
tac	atc	gac	ctg	gca	gct	gat	gag	gaa	ggg	ctt	tgg	gct	gtc	tat	gcc	924	
Tyr	Ile	Asp	Leu	Ala	Ala	Asp	Glu	Glu	Gly	Leu	Trp	Ala	Val	Tyr	Ala		
		275					280					285					
acc	cgg	gag	gat	gac	agg	cac	ttg	tgt	ctg	gcc	aag	tta	gat	cca	cag	972	
Thr	Arg	Glu	Asp	Asp	Arg	His	Leu	Cys	Leu	Ala	Lys	Leu	Asp	Pro	Gln		
		290				295					300						
aca	ctg	gac	aca	gag	cag	cag	tgg	gac	aca	cca	tgt	ccc	aga	gag	aat	1020	
Thr	Leu	Asp	Thr	Glu	Gln	Gln	Trp	Asp	Thr	Pro	Cys	Pro	Arg	Glu	Asn		
305					310					315					320		
gct	gag	gct	gcc	ttt	gtc	atc	tgt	ggg	acc	ctc	tat	gtc	gtc	tat	aac	1068	

Ala Glu Ala Ala Phe Val Ile Cys Gly Thr Leu Tyr Val Val Tyr Asn	
325 330 335	
acc cgt cct gcc agt cgg gcc cgc atc cag tgc tcc ttt gat gcc agc	1116
Thr Arg Pro Ala Ser Arg Ala Arg Ile Gln Cys Ser Phe Asp Ala Ser	
340 345 350	
ggc acc ctg acc cct gaa cgg gca gca ctc cct tat ttt ccc cgc aga	1164
Gly Thr Leu Thr Pro Glu Arg Ala Ala Leu Pro Tyr Phe Pro Arg Arg	
355 360 365	
tat ggt gcc cat gcc agc ctc cgc tat aac ccc cga gaa cgc cag ctc	1212
Tyr Gly Ala His Ala Ser Leu Arg Tyr Asn Pro Arg Glu Arg Gln Leu	
370 375 380	
tat gcc tgg gat gat ggc tac cag att gtc tat aag ctg gag atg agg	1260
Tyr Ala Trp Asp Asp Gly Tyr Gln Ile Val Tyr Lys Leu Glu Met Arg	
385 390 395 400	
aag aaa gag gag gag gtt tga ggagctagcc ttgttttttg catctttctc	1311
Lys Lys Glu Glu Val	
405	
actcccatatc atttatatta tatccccact aaattttcttg ttccctcattc ttcaaagtgtg	1371
ggccagttgt ggctcaaatac ctctatatatt ttagccaatg gcaatcaaatac tctttcagct	1431
cctttgtttc atacggaact ccagatcctg agtaatcctt ttagagcccg aagagtcaaa	1491
accctcaatg ttccctcctg ctctcctgcc ccatgtcaac aaatttcagg ctaaggatgc	1551
cccagaccca gggctctaac cttgtatgag ggcaggccca gggagcaggc agcagtgttc	1611
ttccccctcag agtgacttgg ggagggagaa ataggaggag acgtccagct ctgtcctctc	1671
ttccctcactc ctcccttcag tgtcctgagg aacaggactt tctccacatt gttttgtatt	1731
gcaacatttt gcattaaaag gaaaatccac tgctaaaaaa aaaaaaaaaa aaaaaaaaaa	1791
a	1792

<210> 38
 <211> 406
 <212> PRT
 <213> human

<400> 38

Met Gly Pro Ser Thr Pro Leu Leu Ile Leu Phe Leu Leu Ser Trp Ser
1 5 10 15

Gly Pro Leu Gln Gly Gln Gln His His Leu Val Glu Tyr Met Glu Arg
20 25 30

Arg Leu Ala Ala Leu Glu Glu Arg Leu Ala Gln Cys Gln Asp Gln Ser
35 40 45

Ser Arg His Ala Ala Glu Leu Arg Asp Phe Lys Asn Lys Met Leu Pro
 50 55 60

Leu Leu Glu Val Ala Glu Lys Glu Arg Glu Ala Leu Arg Thr Glu Ala
 65 70 75 80

Asp Thr Ile Ser Gly Arg Val Asp Arg Leu Glu Arg Glu Val Asp Tyr
 85 90 95

Leu Glu Thr Gln Asn Pro Ala Leu Pro Cys Val Glu Phe Asp Glu Lys
 100 105 110

Val Thr Gly Gly Pro Gly Thr Lys Gly Lys Gly Arg Arg Asn Glu Lys
 115 120 125

Tyr Asp Met Val Thr Asp Cys Gly Tyr Thr Ile Ser Gln Val Arg Ser
 130 135 140

Met Lys Ile Leu Lys Arg Phe Gly Gly Pro Ala Gly Leu Trp Thr Lys
 145 150 155 160

Asp Pro Leu Gly Gln Thr Glu Lys Ile Tyr Val Leu Asp Gly Thr Gln
 165 170 175

Asn Asp Thr Ala Phe Val Phe Pro Arg Leu Arg Asp Phe Thr Leu Ala
 180 185 190

Met Ala Ala Arg Lys Ala Ser Arg Val Arg Val Pro Phe Pro Trp Val
 195 200 205

Gly Thr Gly Gln Leu Val Tyr Gly Gly Phe Leu Tyr Phe Ala Arg Arg
 210 215 220

Pro Pro Gly Arg Pro Gly Gly Gly Gly Glu Met Glu Asn Thr Leu Gln
 225 230 235 240

Leu Ile Lys Phe His Leu Ala Asn Arg Thr Val Val Asp Ser Ser Val
 245 250 255

Phe Pro Ala Glu Gly Leu Ile Pro Pro Tyr Gly Leu Thr Ala Asp Thr
 260 265 270

Tyr Ile Asp Leu Ala Ala Asp Glu Glu Gly Leu Trp Ala Val Tyr Ala
 275 280 285

Thr Arg Glu Asp Asp Arg His Leu Cys Leu Ala Lys Leu Asp Pro Gln
 290 295 300

Thr Leu Asp Thr Glu Gln Gln Trp Asp Thr Pro Cys Pro Arg Glu Asn
 305 310 315 320

Ala Glu Ala Ala Phe Val Ile Cys Gly Thr Leu Tyr Val Val Tyr Asn
 325 330 335

Thr Arg Pro Ala Ser Arg Ala Arg Ile Gln Cys Ser Phe Asp Ala Ser
 340 345 350

Gly Thr Leu Thr Pro Glu Arg Ala Ala Leu Pro Tyr Phe Pro Arg Arg
 355 360 365

Tyr Gly Ala His Ala Ser Leu Arg Tyr Asn Pro Arg Glu Arg Gln Leu
 370 375 380

Tyr Ala Trp Asp Asp Gly Tyr Gln Ile Val Tyr Lys Leu Glu Met Arg
 385 390 395 400

Lys Lys Glu Glu Glu Val
 405

<210> 39
 <211> 1925
 <212> DNA
 <213> human

<220>
 <221> CDS
 <222> (127)..(1278)

<400> 39
 agtggagtg gacaggtata taaaggaagt acagggcctg gggaagaggc cctgtctagg 60
 tagctggcac caggagccgt gggcaaggga agaggccaca ccctgccctg ctctgctgca 120
 gccaga atg ggt gtg aag gcg tct caa aca ggc ttt gtg gtc ctg gtg 168
 Met Gly Val Lys Ala Ser Gln Thr Gly Phe Val Val Leu Val
 1 5 10
 ctg ctc cag tgc tgc tct gca tac aaa ctg gtc tgc tac tac acc agc 216
 Leu Leu Gln Cys Cys Ser Ala Tyr Lys Leu Val Cys Tyr Tyr Thr Ser
 15 20 25 30
 tgg tcc cag tac cgg gaa ggc gat ggg agc tgc ttc cca gat gcc ctt 264
 Trp Ser Gln Tyr Arg Glu Gly Asp Gly Ser Cys Phe Pro Asp Ala Leu
 35 40 45

gac cgc ttc ctc tgt acc cac atc atc tac agc ttt gcc aat ata agc	312
Asp Arg Phe Leu Cys Thr His Ile Ile Tyr Ser Phe Ala Asn Ile Ser	
50 55 60	
aac gat cac atc gac acc tgg gag tgg aat gat gtg acg ctc tac ggc	360
Asn Asp His Ile Asp Thr Trp Glu Trp Asn Asp Val Thr Leu Tyr Gly	
65 70 75	
atg ctc aac aca ctc aag aac agg aac ccc aac ctg aag act ctc ttg	408
Met Leu Asn Thr Leu Lys Asn Arg Asn Pro Asn Leu Lys Thr Leu Leu	
80 85 90	
tct gtc gga gga tgg aac ttt ggg tct caa aga ttt tcc aag ata gcc	456
Ser Val Gly Gly Trp Asn Phe Gly Ser Gln Arg Phe Ser Lys Ile Ala	
95 100 105 110	
tcc aac acc cag agt cgc cgg act ttc atc aag tca gta ccg cca ttc	504
Ser Asn Thr Gln Ser Arg Arg Thr Phe Ile Lys Ser Val Pro Pro Phe	
115 120 125	
ctg cgc acc cat ggc ttt gat ggg ctg gac ctt gcc tgg ctc tac cct	552
Leu Arg Thr His Gly Phe Asp Gly Leu Asp Leu Ala Trp Leu Tyr Pro	
130 135 140	
gga cgg aga gac aaa cag cat ttt acc acc cta atc aag gaa atg aag	600
Gly Arg Arg Asp Lys Gln His Phe Thr Thr Leu Ile Lys Glu Met Lys	
145 150 155	
gcc gaa ttt ata aag gaa gcc cag cca ggg aaa aag cag ctc ctg ctc	648
Ala Glu Phe Ile Lys Glu Ala Gln Pro Gly Lys Lys Gln Leu Leu Leu	
160 165 170	
agc gca gca ctg tct gcg ggg aag gtc acc att gac agc agc tat gac	696
Ser Ala Ala Leu Ser Ala Gly Lys Val Thr Ile Asp Ser Ser Tyr Asp	
175 180 185 190	
att gcc aag ata tcc caa cac ctg gat ttc att agc atc atg acc tac	744
Ile Ala Lys Ile Ser Gln His Leu Asp Phe Ile Ser Ile Met Thr Tyr	
195 200 205	
gat ttt cat gga gcc tgg cgt ggg acc aca ggc cat cac agt ccc ctg	792
Asp Phe His Gly Ala Trp Arg Gly Thr Thr Gly His His Ser Pro Leu	
210 215 220	
ttc cga ggt cag gag gat gca agt cct gac aga ttc agc aac act gac	840
Phe Arg Gly Gln Glu Asp Ala Ser Pro Asp Arg Phe Ser Asn Thr Asp	
225 230 235	
tat gct gtg ggg tac atg ttg agg ctg ggg gct cct gcc agt aag ctg	888
Tyr Ala Val Gly Tyr Met Leu Arg Leu Gly Ala Pro Ala Ser Lys Leu	
240 245 250	
gtg atg ggc atc ccc acc ttc ggg agg agc ttc act ctg gct tct tct	936
Val Met Gly Ile Pro Thr Phe Gly Arg Ser Phe Thr Leu Ala Ser Ser	
255 260 265 270	
gag act ggt gtt gga gcc cca atc tca gga ccg gga att cca ggc cgg	984
Glu Thr Gly Val Gly Ala Pro Ile Ser Gly Pro Gly Ile Pro Gly Arg	
275 280 285	

ttc acc aag gag gca ggg acc ctt gcc tac tat gag atc tgt gac ttc	1032
Phe Thr Lys Glu Ala Gly Thr Leu Ala Tyr Tyr Glu Ile Cys Asp Phe	
290 295 300	
ctc cgc gga gcc aca gtc cat aga acc ctc ggc cag cag gtc ccc tat	1080
Leu Arg Gly Ala Thr Val His Arg Thr Leu Gly Gln Gln Val Pro Tyr	
305 310 315	
gcc acc aag ggc aac cag tgg gta gga tac gac gac cag gaa agc gtc	1128
Ala Thr Lys Gly Asn Gln Trp Val Gly Tyr Asp Asp Gln Glu Ser Val	
320 325 330	
aaa agc aag gtg cag tac ctg aag gat agg cag ctg gca ggc gcc atg	1176
Lys Ser Lys Val Gln Tyr Leu Lys Asp Arg Gln Leu Ala Gly Ala Met	
335 340 345 350	
gta tgg gcc ctg gac ctg gat gac ttc cag ggc tcc ttc tgc ggc cag	1224
Val Trp Ala Leu Asp Leu Asp Asp Phe Gln Gly Ser Phe Cys Gly Gln	
355 360 365	
gat ctg cgc ttc cct ctc acc aat gcc atc aag gat gca ctc gct gca	1272
Asp Leu Arg Phe Pro Leu Thr Asn Ala Ile Lys Asp Ala Leu Ala Ala	
370 375 380	
acg tag ccctctgttc tgcacacagc acggggggcca aggatgcccc gtccccctct	1328
Thr	
ggctccagct ggccgggagc ctgatcacct gccctgctga gtcccaggct gagcctcagt	1388
ctccctccct tggggcctat gcagagggtcc acaacacaca gatttgagct cagccctggt	1448
gggcagagag gtagggatgg ggctgtgggg atagtgaggc atcgcaatgt aagactcggg	1508
attagtacac acttgttgat gattaatgga aatgtttaca gatccccaag cctggcaagg	1568
gaatttcttc aactccctgc ccctagccc tccttatcaa aggacaccat tttggcaagc	1628
tctatcacca aggagccaaa catcctacaa gacacagtga ccataactaat tataccccct	1688
gcaaagccag cttgaaacct tcacttagga acgtaatcgt gtcccctatc ctacttcccc	1748
ttcctaattc cacagctgct caataaagta caagagttta acagtgtgtt ggcgctttgc	1808
tttgggtctat ctttgagcgc ccactagacc cactggactc acctccccca tctcttctgg	1868
gttccttcct ctgagccttg ggaccctga gcttgcagag atgaaggccg ccatgtt	1925
<210> 40	
<211> 383	
<212> PRT	
<213> human	
<400> 40	
Met Gly Val Lys Ala Ser Gln Thr Gly Phe Val Val Leu Val Leu Leu	
1 5 10 15	

Gln Cys Cys Ser Ala Tyr Lys Leu Val Cys Tyr Tyr Thr Ser Trp Ser
 20 25 30

Gln Tyr Arg Glu Gly Asp Gly Ser Cys Phe Pro Asp Ala Leu Asp Arg
 35 40 45

Phe Leu Cys Thr His Ile Ile Tyr Ser Phe Ala Asn Ile Ser Asn Asp
 50 55 60

His Ile Asp Thr Trp Glu Trp Asn Asp Val Thr Leu Tyr Gly Met Leu
 65 70 75 80

Asn Thr Leu Lys Asn Arg Asn Pro Asn Leu Lys Thr Leu Leu Ser Val
 85 90 95

Gly Gly Trp Asn Phe Gly Ser Gln Arg Phe Ser Lys Ile Ala Ser Asn
 100 105 110

Thr Gln Ser Arg Arg Thr Phe Ile Lys Ser Val Pro Pro Phe Leu Arg
 115 120 125

Thr His Gly Phe Asp Gly Leu Asp Leu Ala Trp Leu Tyr Pro Gly Arg
 130 135 140

Arg Asp Lys Gln His Phe Thr Thr Leu Ile Lys Glu Met Lys Ala Glu
 145 150 155 160

Phe Ile Lys Glu Ala Gln Pro Gly Lys Lys Gln Leu Leu Leu Ser Ala
 165 170 175

Ala Leu Ser Ala Gly Lys Val Thr Ile Asp Ser Ser Tyr Asp Ile Ala
 180 185 190

Lys Ile Ser Gln His Leu Asp Phe Ile Ser Ile Met Thr Tyr Asp Phe
 195 200 205

His Gly Ala Trp Arg Gly Thr Thr Gly His His Ser Pro Leu Phe Arg
 210 215 220

Gly Gln Glu Asp Ala Ser Pro Asp Arg Phe Ser Asn Thr Asp Tyr Ala
 225 230 235 240

Val Gly Tyr Met Leu Arg Leu Gly Ala Pro Ala Ser Lys Leu Val Met
 245 250 255

Gly Ile Pro Thr Phe Gly Arg Ser Phe Thr Leu Ala Ser Ser Glu Thr
 260 265 270

Gly Val Gly Ala Pro Ile Ser Gly Pro Gly Ile Pro Gly Arg Phe Thr
 275 280 285

Lys Glu Ala Gly Thr Leu Ala Tyr Tyr Glu Ile Cys Asp Phe Leu Arg
 290 295 300

Gly Ala Thr Val His Arg Thr Leu Gly Gln Gln Val Pro Tyr Ala Thr
 305 310 315 320

Lys Gly Asn Gln Trp Val Gly Tyr Asp Asp Gln Glu Ser Val Lys Ser
 325 330 335

Lys Val Gln Tyr Leu Lys Asp Arg Gln Leu Ala Gly Ala Met Val Trp
 340 345 350

Ala Leu Asp Leu Asp Asp Phe Gln Gly Ser Phe Cys Gly Gln Asp Leu
 355 360 365

Arg Phe Pro Leu Thr Asn Ala Ile Lys Asp Ala Leu Ala Ala Thr
 370 375 380

<210> 41
 <211> 2105
 <212> DNA
 <213> human

<220>
 <221> CDS
 <222> (235)..(1752)

<400> 41
 gtcccagctc gggagcacat cagaggctta gaggcgagtg ggaagggact cagacagtgc 60
 aggacgagaa acgcccgcgg caccaaagcc cctcagagcg tcgccccgc ctctagttct 120
 agaaagtcag tttcccggca ctggcacccc ggaacctcag gggctgccga gctggggggg 180
 cgctcaagct gcgaggatcc gggctgcccg cgagacgagg agcgggccc cagg atg 237
 Met
 1
 ggg tgc atg aag tcc aag ttc ctc cag gtc gga ggc aat aca ttc tca 285
 Gly Cys Met Lys Ser Lys Phe Leu Gln Val Gly Gly Asn Thr Phe Ser
 5 10 15
 aaa act gaa acc agc gcc agc cca cac tgt cct gtg tac gtg ccg gat 333
 Lys Thr Glu Thr Ser Ala Ser Pro His Cys Pro Val Tyr Val Pro Asp
 20 25 30

ccc aca tcc acc atc aag ccg ggg cct aat agc cac aac agc aac aca	381
Pro Thr Ser Thr Ile Lys Pro Gly Pro Asn Ser His Asn Ser Asn Thr	
35 40 45	
cca gga atc agg gag gca ggc tct gag gac atc atc gtg gtt gcc ctg	429
Pro Gly Ile Arg Glu Ala Gly Ser Glu Asp Ile Ile Val Val Ala Leu	
50 55 60 65	
tat gat tac gag gcc att cac cac gaa gac ctc agc ttc cag aag ggg	477
Tyr Asp Tyr Glu Ala Ile His His Glu Asp Leu Ser Phe Gln Lys Gly	
70 75 80	
gac cag atg gtg gtc cta gag gaa tcc ggg gag tgg tgg aag gct cga	525
Asp Gln Met Val Val Leu Glu Glu Ser Gly Glu Trp Trp Lys Ala Arg	
85 90 95	
tcc ctg gcc acc cgg aag gag ggc tac atc cca agc aac tat gtc gcc	573
Ser Leu Ala Thr Arg Lys Glu Gly Tyr Ile Pro Ser Asn Tyr Val Ala	
100 105 110	
cgc gtt gac tct ctg gag aca gag gag tgg ttt ttc aag ggc atc agc	621
Arg Val Asp Ser Leu Glu Thr Glu Glu Trp Phe Phe Lys Gly Ile Ser	
115 120 125	
cgg aag gac gca gag cgc caa ctg ctg gct ccc ggc aac atg ctg ggc	669
Arg Lys Asp Ala Glu Arg Gln Leu Leu Ala Pro Gly Asn Met Leu Gly	
130 135 140 145	
tcc ttc atg atc cgg gat agc gag acc act aaa gga agc tac tct ttg	717
Ser Phe Met Ile Arg Asp Ser Glu Thr Thr Lys Gly Ser Tyr Ser Leu	
150 155 160	
tcc gtg cga gac tac gac cct cgg cag gga gat acc gtg aaa cat tac	765
Ser Val Arg Asp Tyr Asp Pro Arg Gln Gly Asp Thr Val Lys His Tyr	
165 170 175	
aag atc cgg acc ctg gac aac ggg ggc ttc tac ata tcc ccc cga agc	813
Lys Ile Arg Thr Leu Asp Asn Gly Gly Phe Tyr Ile Ser Pro Arg Ser	
180 185 190	
acc ttc agc act ctg cag gag ctg gtg gac cac tac aag aag ggg aac	861
Thr Phe Ser Thr Leu Gln Glu Leu Val Asp His Tyr Lys Lys Gly Asn	
195 200 205	
gac ggg ctc tgc cag aaa ctg tcg gtg ccc tgc atg tct tcc aag ccc	909
Asp Gly Leu Cys Gln Lys Leu Ser Val Pro Cys Met Ser Ser Lys Pro	
210 215 220 225	
cag aag cct tgg gag aaa gat gcc tgg gag atc cct cgg gaa tcc ctc	957
Gln Lys Pro Trp Glu Lys Asp Ala Trp Glu Ile Pro Arg Glu Ser Leu	
230 235 240	
aag ctg gag aag aaa ctt gga gct ggg cag ttt ggg gaa gtc tgg atg	1005
Lys Leu Glu Lys Lys Leu Gly Ala Gly Gln Phe Gly Glu Val Trp Met	
245 250 255	
gcc acc tac aac aag cac acc aag gtg gca gtg aag acg atg aag cca	1053
Ala Thr Tyr Asn Lys His Thr Lys Val Ala Val Lys Thr Met Lys Pro	
260 265 270	

ggg agc atg tcg gtg gag gcc ttc ctg gca gag gcc aac gtg atg aaa Gly Ser Met Ser Val Glu Ala Phe Leu Ala Glu Ala Asn Val Met Lys 275 280 285	1101
act ctg cag cat gac aag ctg gtc aaa ctt cat gcg gtg gtc acc aag Thr Leu Gln His Asp Lys Leu Val Lys Leu His Ala Val Val Thr Lys 290 295 300 305	1149
gag ccc atc tac atc atc acg gag ttc atg gcc aaa gga agc ttg ctg Glu Pro Ile Tyr Ile Ile Thr Glu Phe Met Ala Lys Gly Ser Leu Leu 310 315 320	1197
gac ttt ctg aaa agt gat gag ggc agc aag cag cca ttg cca aaa ctc Asp Phe Leu Lys Ser Asp Glu Gly Ser Lys Gln Pro Leu Pro Lys Leu 325 330 335	1245
att gac ttc tca gcc cag att gca gaa ggc atg gcc ttc atc gag cag Ile Asp Phe Ser Ala Gln Ile Ala Glu Gly Met Ala Phe Ile Glu Gln 340 345 350	1293
agg aac tac atc cac cga gac ctc cga gct gcc aac atc ttg gtc tct Arg Asn Tyr Ile His Arg Asp Leu Arg Ala Ala Asn Ile Leu Val Ser 355 360 365	1341
gca tcc ctg gtg tgt aag att gct gac ttt ggc ctg gcc cgg gtc att Ala Ser Leu Val Cys Lys Ile Ala Asp Phe Gly Leu Ala Arg Val Ile 370 375 380 385	1389
gag gac aac gag tac acg gct cgg gaa ggg gcc aag ttc ccc atc aag Glu Asp Asn Glu Tyr Thr Ala Arg Glu Gly Ala Lys Phe Pro Ile Lys 390 395 400	1437
tgg aca gct cct gaa gcc atc aac ttt ggc tcc ttc acc atc aag tca Trp Thr Ala Pro Glu Ala Ile Asn Phe Gly Ser Phe Thr Ile Lys Ser 405 410 415	1485
gac gtc tgg tcc ttt ggt atc ctg ctg atg gag atc gtc acc tac ggc Asp Val Trp Ser Phe Gly Ile Leu Leu Met Glu Ile Val Thr Tyr Gly 420 425 430	1533
cgg atc cct tac cca ggg atg tca aac cct gaa gtg atc cga gct ctg Arg Ile Pro Tyr Pro Gly Met Ser Asn Pro Glu Val Ile Arg Ala Leu 435 440 445	1581
gag cgt gga tac cgg atg cct cgc cca gag aac tgc cca gag gag ctc Glu Arg Gly Tyr Arg Met Pro Arg Pro Glu Asn Cys Pro Glu Glu Leu 450 455 460 465	1629
tac aac atc atg atg cgc tgc tgg aaa aac cgt ccg gag gag cgg ccg Tyr Asn Ile Met Met Arg Cys Trp Lys Asn Arg Pro Glu Glu Arg Pro 470 475 480	1677
acc ttc gaa tac atc cag agt gtg ctg gat gac ttc tac acg gcc aca Thr Phe Glu Tyr Ile Gln Ser Val Leu Asp Asp Phe Tyr Thr Ala Thr 485 490 495	1725
gag agc cag tac caa cag cag cca tga tagggaggac cagggcaggg Glu Ser Gln Tyr Gln Gln Gln Pro 500 505	1772

ccagggggtg cccaggtggt ggctgcaagg tggctccagc accatccgcc agggcccaca 1832
 ccccttctc actcccagac accaccctc gcttcagcca cagtttcctc atctgtccag 1892
 tgggtaggtt ggactggaaa atctcttttt gactcttgca atccacaatc tgacattctc 1952
 aggaagcccc caagttgata tttctatttc ctggaatggt tggattttag ttacagctgt 2012
 gatttggaag ggaaactttc aaaatagtga aatgaatatt taaataaaaag atataaatgc 2072
 caaagtcttt accaaaaaaaa aaaaaaaaaaa aaa 2105

<210> 42
 <211> 505
 <212> PRT
 <213> human

<400> 42

Met Gly Cys Met Lys Ser Lys Phe Leu Gln Val Gly Gly Asn Thr Phe
 1 5 10 15

Ser Lys Thr Glu Thr Ser Ala Ser Pro His Cys Pro Val Tyr Val Pro
 20 25 30

Asp Pro Thr Ser Thr Ile Lys Pro Gly Pro Asn Ser His Asn Ser Asn
 35 40 45

Thr Pro Gly Ile Arg Glu Ala Gly Ser Glu Asp Ile Ile Val Val Ala
 50 55 60

Leu Tyr Asp Tyr Glu Ala Ile His His Glu Asp Leu Ser Phe Gln Lys
 65 70 75 80

Gly Asp Gln Met Val Val Leu Glu Glu Ser Gly Glu Trp Trp Lys Ala
 85 90 95

Arg Ser Leu Ala Thr Arg Lys Glu Gly Tyr Ile Pro Ser Asn Tyr Val
 100 105 110

Ala Arg Val Asp Ser Leu Glu Thr Glu Glu Trp Phe Phe Lys Gly Ile
 115 120 125

Ser Arg Lys Asp Ala Glu Arg Gln Leu Leu Ala Pro Gly Asn Met Leu
 130 135 140

Gly Ser Phe Met Ile Arg Asp Ser Glu Thr Thr Lys Gly Ser Tyr Ser
 145 150 155 160

Leu Ser Val Arg Asp Tyr Asp Pro Arg Gln Gly Asp Thr Val Lys His
 165 170 175

Tyr Lys Ile Arg Thr Leu Asp Asn Gly Gly Phe Tyr Ile Ser Pro Arg
 180 185 190

Ser Thr Phe Ser Thr Leu Gln Glu Leu Val Asp His Tyr Lys Lys Gly
 195 200 205

Asn Asp Gly Leu Cys Gln Lys Leu Ser Val Pro Cys Met Ser Ser Lys
 210 215 220

Pro Gln Lys Pro Trp Glu Lys Asp Ala Trp Glu Ile Pro Arg Glu Ser
 225 230 235 240

Leu Lys Leu Glu Lys Lys Leu Gly Ala Gly Gln Phe Gly Glu Val Trp
 245 250 255

Met Ala Thr Tyr Asn Lys His Thr Lys Val Ala Val Lys Thr Met Lys
 260 265 270

Pro Gly Ser Met Ser Val Glu Ala Phe Leu Ala Glu Ala Asn Val Met
 275 280 285

Lys Thr Leu Gln His Asp Lys Leu Val Lys Leu His Ala Val Val Thr
 290 295 300

Lys Glu Pro Ile Tyr Ile Ile Thr Glu Phe Met Ala Lys Gly Ser Leu
 305 310 315 320

Leu Asp Phe Leu Lys Ser Asp Glu Gly Ser Lys Gln Pro Leu Pro Lys
 325 330 335

Leu Ile Asp Phe Ser Ala Gln Ile Ala Glu Gly Met Ala Phe Ile Glu
 340 345 350

Gln Arg Asn Tyr Ile His Arg Asp Leu Arg Ala Ala Asn Ile Leu Val
 355 360 365

Ser Ala Ser Leu Val Cys Lys Ile Ala Asp Phe Gly Leu Ala Arg Val
 370 375 380

Ile Glu Asp Asn Glu Tyr Thr Ala Arg Glu Gly Ala Lys Phe Pro Ile
 385 390 395 400

Lys Trp Thr Ala Pro Glu Ala Ile Asn Phe Gly Ser Phe Thr Ile Lys
405 410 415

Ser Asp Val Trp Ser Phe Gly Ile Leu Leu Met Glu Ile Val Thr Tyr
420 425 430

Gly Arg Ile Pro Tyr Pro Gly Met Ser Asn Pro Glu Val Ile Arg Ala
435 440 445

Leu Glu Arg Gly Tyr Arg Met Pro Arg Pro Glu Asn Cys Pro Glu Glu
450 455 460

Leu Tyr Asn Ile Met Met Arg Cys Trp Lys Asn Arg Pro Glu Glu Arg
465 470 475 480

Pro Thr Phe Glu Tyr Ile Gln Ser Val Leu Asp Asp Phe Tyr Thr Ala
485 490 495

Thr Glu Ser Gln Tyr Gln Gln Gln Pro
500 505

<210> 43
<211> 3432
<212> DNA
<213> human

<220>
<221> CDS
<222> (248)..(2572)

<400> 43
actccagcgc gcggctacct acgcttggtg cttgctttct ccagccatcg gagaccagag 60
ccgccccctc tgctcgagaa aggggctcag cgggcgcgga agcggagggg gaccaccgtg 120
gagagcgcggtg tcccagcccc gccactgcgg atccctgaaa ccaaaaagct cctgctgctt 180
ctgtacccccg cctgtccctc ccagctgcgc agggccccctt cgtgggatca tcagcccga 240
gacaggg atg gag agg cct ctg tgc tcc cac ctc tgc agc tgc ctg gct 289
Met Glu Arg Pro Leu Cys Ser His Leu Cys Ser Cys Leu Ala
1 5 10
atg ctg gcc ctc ctg tcc ccc ctg agc ctg gca cag tat gac agc tgg 337
Met Leu Ala Leu Leu Ser Pro Leu Ser Leu Ala Gln Tyr Asp Ser Trp
15 20 25 30
ccc cat tac ccc gag tac ttc cag caa ccg gct cct gag tat cac cag 385
Pro His Tyr Pro Glu Tyr Phe Gln Gln Pro Ala Pro Glu Tyr His Gln
35 40 45

ccc cag gcc ccc gcc aac gtg gcc aag att cag ctg cgc ctg gct ggg Pro Gln Ala Pro Ala Asn Val Ala Lys Ile Gln Leu Arg Leu Ala Gly 50 55 60	433
cag aag agg aag cac agc gag ggc cgg gtg gag gtg tac tat gat ggc Gln Lys Arg Lys His Ser Glu Gly Arg Val Glu Val Tyr Tyr Asp Gly 65 70 75	481
cag tgg ggc acc gtg tgc gat gac gac ttc tcc atc cac gct gcc cac Gln Trp Gly Thr Val Cys Asp Asp Asp Phe Ser Ile His Ala Ala His 80 85 90	529
gtc gtc tgc cgg gag ctg ggc tat gtg gag gcc aag tcc tgg act gcc Val Val Cys Arg Glu Leu Gly Tyr Val Glu Ala Lys Ser Trp Thr Ala 95 100 105 110	577
agc tcc tcc tac ggc aag gga gaa ggg ccc atc tgg tta gac aat ctc Ser Ser Ser Tyr Gly Lys Gly Glu Gly Pro Ile Trp Leu Asp Asn Leu 115 120 125	625
cac tgt act ggc aac gag gcg acc ctt gca gca tgc acc tcc aat ggc His Cys Thr Gly Asn Glu Ala Thr Leu Ala Ala Cys Thr Ser Asn Gly 130 135 140	673
tgg ggc gtc act gac tgc aag cac acg gag gat gtc ggt gtg gtg tgc Trp Gly Val Thr Asp Cys Lys His Thr Glu Asp Val Gly Val Val Cys 145 150 155	721
agc gac aaa agg att cct ggg ttc aaa ttt gac aat tcg ttg atc aac Ser Asp Lys Arg Ile Pro Gly Phe Lys Phe Asp Asn Ser Leu Ile Asn 160 165 170	769
cag ata gag aac ctg aat atc cag gtg gag gac att cgg att cga gcc Gln Ile Glu Asn Leu Asn Ile Gln Val Glu Asp Ile Arg Ile Arg Ala 175 180 185 190	817
atc ctc tca acc tac cgc aag cgc acc cca gtg atg gag ggc tac gtg Ile Leu Ser Thr Tyr Arg Lys Arg Thr Pro Val Met Glu Gly Tyr Val 195 200 205	865
gag gtg aag gag ggc aag acc tgg aag cag atc tgt gac aag cac tgg Glu Val Lys Glu Gly Lys Thr Trp Lys Gln Ile Cys Asp Lys His Trp 210 215 220	913
acg gcc aag aat tcc cgc gtg gtc tgc ggc atg ttt ggc ttc cct ggg Thr Ala Lys Asn Ser Arg Val Val Cys Gly Met Phe Gly Phe Pro Gly 225 230 235	961
gag agg aca tac aat acc aaa gtg tac aaa atg ttt gcc tca cgg agg Glu Arg Thr Tyr Asn Thr Lys Val Tyr Lys Met Phe Ala Ser Arg Arg 240 245 250	1009
aag cag cgc tac tgg cca ttc tcc atg gac tgc acc ggc aca gag gcc Lys Gln Arg Tyr Trp Pro Phe Ser Met Asp Cys Thr Gly Thr Glu Ala 255 260 265 270	1057
cac atc tcc agc tgc aag ctg ggc ccc cag gtg tca ctg gac ccc atg His Ile Ser Ser Cys Lys Leu Gly Pro Gln Val Ser Leu Asp Pro Met 275 280 285	1105

aag aat gtc acc tgc gag aat ggg ctg ccg gcc gtg gtg agt tgt gtg	1153
Lys Asn Val Thr Cys Glu Asn Gly Leu Pro Ala Val Val Ser Cys Val	
290 295 300	
cct ggg cag gtc ttc agc cct gac gga ccc tcg aga ttc cgg aaa gca	1201
Pro Gly Gln Val Phe Ser Pro Asp Gly Pro Ser Arg Phe Arg Lys Ala	
305 310 315	
tac aag cca gag caa ccc ctg gtg cga ctg aga ggc ggt gcc tac atc	1249
Tyr Lys Pro Glu Gln Pro Leu Val Arg Leu Arg Gly Gly Ala Tyr Ile	
320 325 330	
ggg gag ggc cgc gtg gag gtg ctc aaa aat gga gaa tgg ggg acc gtc	1297
Gly Glu Gly Arg Val Glu Val Leu Lys Asn Gly Glu Trp Gly Thr Val	
335 340 345 350	
tgc gac gac aag tgg gac ctg gtg tcg gcc agt gtg gtc tgc aga gag	1345
Cys Asp Asp Lys Trp Asp Leu Val Ser Ala Ser Val Val Cys Arg Glu	
355 360 365	
ctg ggc ttt ggg agt gcc aaa gag gca gtc act ggc tcc cga ctg ggg	1393
Leu Gly Phe Gly Ser Ala Lys Glu Ala Val Thr Gly Ser Arg Leu Gly	
370 375 380	
caa ggg atc gga ccc atc cac ctc aac gag atc cag tgc aca ggc aat	1441
Gln Gly Ile Gly Pro Ile His Leu Asn Glu Ile Gln Cys Thr Gly Asn	
385 390 395	
gag aag tcc att ata gac tgc aag ttc aat gcc gag tct cag ggc tgc	1489
Glu Lys Ser Ile Ile Asp Cys Lys Phe Asn Ala Glu Ser Gln Gly Cys	
400 405 410	
aac cac gag gag gat gct ggt gtg aga tgc aac acc cct gcc atg ggc	1537
Asn His Glu Glu Asp Ala Gly Val Arg Cys Asn Thr Pro Ala Met Gly	
415 420 425 430	
ttg cag aag aag ctg cgc ctg aac ggc ggc cgc aat ccc tac gag ggc	1585
Leu Gln Lys Lys Leu Arg Leu Asn Gly Gly Arg Asn Pro Tyr Glu Gly	
435 440 445	
cga gtg gag gtg ctg gtg gag aga aac ggg tcc ctt gtg tgg ggg atg	1633
Arg Val Glu Val Leu Val Glu Arg Asn Gly Ser Leu Val Trp Gly Met	
450 455 460	
gtg tgt ggc caa aac tgg ggc atc gtg gag gcc atg gtg gtc tgc cgc	1681
Val Cys Gly Gln Asn Trp Gly Ile Val Glu Ala Met Val Val Cys Arg	
465 470 475	
cag ctg ggc ctg gga ttc gcc agc aac gcc ttc cag gag acc tgg tat	1729
Gln Leu Gly Leu Gly Phe Ala Ser Asn Ala Phe Gln Glu Thr Trp Tyr	
480 485 490	
tgg cac gga gat gtc aac agc aac aaa gtg gtc atg agt gga gtg aag	1777
Trp His Gly Asp Val Asn Ser Asn Lys Val Val Met Ser Gly Val Lys	
495 500 505 510	
tgc tcg gga acg gag ctg tcc ctg gcg cac tgc cgc cac gac ggg gag	1825
Cys Ser Gly Thr Glu Leu Ser Leu Ala His Cys Arg His Asp Gly Glu	
515 520 525	

gac gtg gcc tgc ccc cag ggc gga gtg cag tac ggg gcc gga gtt gcc Asp Val Ala Cys Pro Gln Gly Gly Val Gln Tyr Gly Ala Gly Val Ala 530 535 540	1873
tgc tca gaa acc gcc cct gac ctg gtc ctc aat gcg gag atg gtg cag Cys Ser Glu Thr Ala Pro Asp Leu Val Leu Asn Ala Glu Met Val Gln 545 550 555	1921
cag acc acc tac ctg gag gac cgg ccc atg ttc atg ctg cag tgt gcc Gln Thr Thr Tyr Leu Glu Asp Arg Pro Met Phe Met Leu Gln Cys Ala 560 565 570	1969
atg gag gag aac tgc ctc tcg gcc tca gcc gcg cag acc gac ccc acc Met Glu Glu Asn Cys Leu Ser Ala Ser Ala Ala Gln Thr Asp Pro Thr 575 580 585 590	2017
acg ggc tac cgc cgg ctc ctg cgc ttc tcc tcc cag atc cac aac aat Thr Gly Tyr Arg Arg Leu Leu Arg Phe Ser Ser Gln Ile His Asn Asn 595 600 605	2065
ggc cag tcc gac ttc cgg ccc aag aac ggc cgc cac gcg tgg atc tgg Gly Gln Ser Asp Phe Arg Pro Lys Asn Gly Arg His Ala Trp Ile Trp 610 615 620	2113
cac gac tgt cac agg cac tac cac agc atg gag gtg ttc acc cac tat His Asp Cys His Arg His Tyr His Ser Met Glu Val Phe Thr His Tyr 625 630 635	2161
gac ctg ctg aac ctc aat ggc acc aag gtg gca gag ggc cac aag gcc Asp Leu Leu Asn Leu Asn Gly Thr Lys Val Ala Glu Gly His Lys Ala 640 645 650	2209
agc ttc tgc ttg gag gac aca gaa tgt gaa gga gac atc cag aag aat Ser Phe Cys Leu Glu Asp Thr Glu Cys Glu Gly Asp Ile Gln Lys Asn 655 660 665 670	2257
tac gag tgt gcc aac ttc ggc gat cag ggc atc acc atg ggc tgc tgg Tyr Glu Cys Ala Asn Phe Gly Asp Gln Gly Ile Thr Met Gly Cys Trp 675 680 685	2305
gac atg tac cgc cat gac atc gac tgc cag tgg gtt gac atc act gac Asp Met Tyr Arg His Asp Ile Asp Cys Gln Trp Val Asp Ile Thr Asp 690 695 700	2353
gtg ccc cct gga gac tac ctg ttc cag gtt gtt att aac ccc aac ttc Val Pro Pro Gly Asp Tyr Leu Phe Gln Val Val Ile Asn Pro Asn Phe 705 710 715	2401
gag gtt gca gaa tcc gat tac tcc aac aac atc atg aaa tgc agg agc Glu Val Ala Glu Ser Asp Tyr Ser Asn Asn Ile Met Lys Cys Arg Ser 720 725 730	2449
cgc tat gac ggc cac cgc atc tgg atg tac aac tgc cac ata ggt ggt Arg Tyr Asp Gly His Arg Ile Trp Met Tyr Asn Cys His Ile Gly Gly 735 740 745 750	2497
tcc ttc agc gaa gag acg gaa aaa aag ttt gag cac ttc agc ggg ctc Ser Phe Ser Glu Glu Thr Glu Lys Lys Phe Glu His Phe Ser Gly Leu 755 760 765	2545

tta aac aac cag ctg tcc ccg cag taa agaagcctgc gtggtcaact 2592
 Leu Asn Asn Gln Leu Ser Pro Gln
 770

cctgtcttca ggccacacca catcttccat gggacttccc cccaacaact gagtctgaac 2652
 gaatgccacg tgccctcacc cagcccggcc cccaccctgt ccagaccctt acagctgtgt 2712
 ctaagctcag gaggaaaggg accctcccat cattcatggg gggctgctac ctgacccttg 2772
 gggcctgaga aggccttggg ggggtggggg ttgtccacag agctgctgga gcagcaccaa 2832
 gagccagtct tgaccgggat gaggcccaca gacaggttgt catcagcttg tcccattcaa 2892
 gccaccgagc tcaccacaga cacagtggag ccgcgctctt ctccagtgc acgtggacaa 2952
 atgcgggctc atcagccccc ccagagaggg tcaggccgaa ccccatcttct cctcctctta 3012
 ggtcattttc agcaaacttg aatatctaga cctctcttcc aatgaaaccc tccagtctat 3072
 tatagtcaca tagataatgg tgccacgtgt tttctgattt ggtgagctca gacttggtgc 3132
 ttccctctcc acaaccccca ccccttgttt ttcaagatac tattattata ttttcacaga 3192
 cttttgaagc acaaatttat tggcatttaa tattggacat ctggggccctt ggaagtacaa 3252
 atctaaggaa aaaccaaccc actgtgtaag tgactcatct tcctgttggt ccaattctgt 3312
 gggtttttga ttcaacggtg ctataaccag ggtcctgggt gacagggcgc tctactgagca 3372
 ccatgtgtca tcacagacac ttacacatac ttgaaacttg gaataaaaga aagatttatg 3432

<210> 44
 <211> 774
 <212> PRT
 <213> human

<400> 44

Met Glu Arg Pro Leu Cys Ser His Leu Cys Ser Cys Leu Ala Met Leu
 1 5 10 15

Ala Leu Leu Ser Pro Leu Ser Leu Ala Gln Tyr Asp Ser Trp Pro His
 20 25 30

Tyr Pro Glu Tyr Phe Gln Gln Pro Ala Pro Glu Tyr His Gln Pro Gln
 35 40 45

Ala Pro Ala Asn Val Ala Lys Ile Gln Leu Arg Leu Ala Gly Gln Lys
 50 55 60

Arg Lys His Ser Glu Gly Arg Val Glu Val Tyr Tyr Asp Gly Gln Trp
 65 70 75 80

Gly Thr Val Cys Asp Asp Asp Phe Ser Ile His Ala Ala His Val Val
 85 90 95
 Cys Arg Glu Leu Gly Tyr Val Glu Ala Lys Ser Trp Thr Ala Ser Ser
 100 105 110
 Ser Tyr Gly Lys Gly Glu Gly Pro Ile Trp Leu Asp Asn Leu His Cys
 115 120 125
 Thr Gly Asn Glu Ala Thr Leu Ala Ala Cys Thr Ser Asn Gly Trp Gly
 130 135 140
 Val Thr Asp Cys Lys His Thr Glu Asp Val Gly Val Val Cys Ser Asp
 145 150 155 160
 Lys Arg Ile Pro Gly Phe Lys Phe Asp Asn Ser Leu Ile Asn Gln Ile
 165 170 175
 Glu Asn Leu Asn Ile Gln Val Glu Asp Ile Arg Ile Arg Ala Ile Leu
 180 185 190
 Ser Thr Tyr Arg Lys Arg Thr Pro Val Met Glu Gly Tyr Val Glu Val
 195 200 205
 Lys Glu Gly Lys Thr Trp Lys Gln Ile Cys Asp Lys His Trp Thr Ala
 210 215 220
 Lys Asn Ser Arg Val Val Cys Gly Met Phe Gly Phe Pro Gly Glu Arg
 225 230 235 240
 Thr Tyr Asn Thr Lys Val Tyr Lys Met Phe Ala Ser Arg Arg Lys Gln
 245 250 255
 Arg Tyr Trp Pro Phe Ser Met Asp Cys Thr Gly Thr Glu Ala His Ile
 260 265 270
 Ser Ser Cys Lys Leu Gly Pro Gln Val Ser Leu Asp Pro Met Lys Asn
 275 280 285
 Val Thr Cys Glu Asn Gly Leu Pro Ala Val Val Ser Cys Val Pro Gly
 290 295 300
 Gln Val Phe Ser Pro Asp Gly Pro Ser Arg Phe Arg Lys Ala Tyr Lys
 305 310 315 320

Pro Glu Gln Pro Leu Val Arg Leu Arg Gly Gly Ala Tyr Ile Gly Glu
 325 330 335

Gly Arg Val Glu Val Leu Lys Asn Gly Glu Trp Gly Thr Val Cys Asp
 340 345 350

Asp Lys Trp Asp Leu Val Ser Ala Ser Val Val Cys Arg Glu Leu Gly
 355 360 365

Phe Gly Ser Ala Lys Glu Ala Val Thr Gly Ser Arg Leu Gly Gln Gly
 370 375 380

Ile Gly Pro Ile His Leu Asn Glu Ile Gln Cys Thr Gly Asn Glu Lys
 385 390 395 400

Ser Ile Ile Asp Cys Lys Phe Asn Ala Glu Ser Gln Gly Cys Asn His
 405 410 415

Glu Glu Asp Ala Gly Val Arg Cys Asn Thr Pro Ala Met Gly Leu Gln
 420 425 430

Lys Lys Leu Arg Leu Asn Gly Gly Arg Asn Pro Tyr Glu Gly Arg Val
 435 440 445

Glu Val Leu Val Glu Arg Asn Gly Ser Leu Val Trp Gly Met Val Cys
 450 455 460

Gly Gln Asn Trp Gly Ile Val Glu Ala Met Val Val Cys Arg Gln Leu
 465 470 475 480

Gly Leu Gly Phe Ala Ser Asn Ala Phe Gln Glu Thr Trp Tyr Trp His
 485 490 495

Gly Asp Val Asn Ser Asn Lys Val Val Met Ser Gly Val Lys Cys Ser
 500 505 510

Gly Thr Glu Leu Ser Leu Ala His Cys Arg His Asp Gly Glu Asp Val
 515 520 525

Ala Cys Pro Gln Gly Gly Val Gln Tyr Gly Ala Gly Val Ala Cys Ser
 530 535 540

Glu Thr Ala Pro Asp Leu Val Leu Asn Ala Glu Met Val Gln Gln Thr
 545 550 555 560

Thr Tyr Leu Glu Asp Arg Pro Met Phe Met Leu Gln Cys Ala Met Glu
565 570 575

Glu Asn Cys Leu Ser Ala Ser Ala Ala Gln Thr Asp Pro Thr Thr Gly
580 585 590

Tyr Arg Arg Leu Leu Arg Phe Ser Ser Gln Ile His Asn Asn Gly Gln
595 600 605

Ser Asp Phe Arg Pro Lys Asn Gly Arg His Ala Trp Ile Trp His Asp
610 615 620

Cys His Arg His Tyr His Ser Met Glu Val Phe Thr His Tyr Asp Leu
625 630 635 640

Leu Asn Leu Asn Gly Thr Lys Val Ala Glu Gly His Lys Ala Ser Phe
645 650 655

Cys Leu Glu Asp Thr Glu Cys Glu Gly Asp Ile Gln Lys Asn Tyr Glu
660 665 670

Cys Ala Asn Phe Gly Asp Gln Gly Ile Thr Met Gly Cys Trp Asp Met
675 680 685

Tyr Arg His Asp Ile Asp Cys Gln Trp Val Asp Ile Thr Asp Val Pro
690 695 700

Pro Gly Asp Tyr Leu Phe Gln Val Val Ile Asn Pro Asn Phe Glu Val
705 710 715 720

Ala Glu Ser Asp Tyr Ser Asn Asn Ile Met Lys Cys Arg Ser Arg Tyr
725 730 735

Asp Gly His Arg Ile Trp Met Tyr Asn Cys His Ile Gly Gly Ser Phe
740 745 750

Ser Glu Glu Thr Glu Lys Lys Phe Glu His Phe Ser Gly Leu Leu Asn
755 760 765

Asn Gln Leu Ser Pro Gln
770

<210> 45
<211> 3543
<212> DNA
<213> human

<220>
 <221> CDS
 <222> (373)..(3003)

<400> 45
 ccccggaac aggaaccctg gtggacgggt cccagcaggc ttcttcggtg cccgagaggg 60
 agcgggtgcc caagggggtg gtccctgtgg cagggtcccgg ggtgggggcg cggcgctccg 120
 ggaagagcct tccgcaggtc cccgccccgt cacgtgggcg ccggccccgg ccgctgcggt 180
 cgggtccgctg gttggtcggg cgcttggtcc ggcagttggt cgggtgggcca gtggcccgtc 240
 gctcgcttct gggctctcat gtttgaaggt gggagggaca cgggagcggc ccgcacacct 300
 gagccgccccg gagaggagcc tcggccccgt acccagtaag aagaggagga ggccaggcag 360
 gcaaaaggag tc atg gct tct gat gct agt cat gcg ctg gaa gct gcc ctg 411
 Met Ala Ser Asp Ala Ser His Ala Leu Glu Ala Ala Leu
 1 5 10
 gag caa atg gac ggg atc att gca ggc act aaa aca ggt gca gat ctt 459
 Glu Gln Met Asp Gly Ile Ile Ala Gly Thr Lys Thr Gly Ala Asp Leu
 15 20 25
 agt gat ggt act tgt gag cct gga ctg gct tcc ccg gcc tcc tac atg 507
 Ser Asp Gly Thr Cys Glu Pro Gly Leu Ala Ser Pro Ala Ser Tyr Met
 30 35 40 45
 aac ccc ttc ccg gtg ctc cat ctc atc gag gac ttg agg ctg gcc ttg 555
 Asn Pro Phe Pro Val Leu His Leu Ile Glu Asp Leu Arg Leu Ala Leu
 50 55 60
 gag atg ctg gag ctt cct cag gag aga gca gcc ctc ctg agc cag atc 603
 Glu Met Leu Glu Leu Pro Gln Glu Arg Ala Ala Leu Leu Ser Gln Ile
 65 70 75
 cct ggc cca aca gct gcc tac ata aag gaa tgg ttt gaa gag agc ttg 651
 Pro Gly Pro Thr Ala Ala Tyr Ile Lys Glu Trp Phe Glu Glu Ser Leu
 80 85 90
 tcc cag gta aac cac cac agt gct gct agt aat gaa acc tac cag gaa 699
 Ser Gln Val Asn His His Ser Ala Ala Ser Asn Glu Thr Tyr Gln Glu
 95 100 105
 cgc ttg gca cgt cta gaa ggg gat aag gag tcc ctc ata ttg cag gtg 747
 Arg Leu Ala Arg Leu Glu Gly Asp Lys Glu Ser Leu Ile Leu Gln Val
 110 115 120 125
 agt gtc ctc aca gac caa gta gaa gcc cag gga gaa aag att cga gac 795
 Ser Val Leu Thr Asp Gln Val Glu Ala Gln Gly Glu Lys Ile Arg Asp
 130 135 140
 ctg gaa gtg tgt ctg gaa gga cac cag gtg aaa ctc aat gct gct gaa 843
 Leu Glu Val Cys Leu Glu Gly His Gln Val Lys Leu Asn Ala Ala Glu
 145 150 155
 gag atg ctt caa cag gag ctg cta agc cgc aca tct ctt gag acc cag 891

Glu	Met	Leu	Gln	Gln	Glu	Leu	Leu	Ser	Arg	Thr	Ser	Leu	Glu	Thr	Gln		
		160					165					170					
aag	ctc	gat	ctg	atg	act	gaa	gtg	tct	gag	ctg	aag	ctc	aag	ctg	gtt	939	
Lys	Leu	Asp	Leu	Met	Thr	Glu	Val	Ser	Glu	Leu	Lys	Leu	Lys	Leu	Val		
	175					180					185						
ggc	atg	gag	aag	gag	cag	aga	gag	cag	gag	gag	aag	cag	aga	aaa	gca	987	
Gly	Met	Glu	Lys	Glu	Gln	Arg	Glu	Gln	Glu	Glu	Lys	Gln	Arg	Lys	Ala		
190					195					200					205		
gag	gag	tta	ctg	caa	gag	ctc	agg	cac	ctc	aaa	atc	aaa	gtg	gaa	gag	1035	
Glu	Glu	Leu	Leu	Gln	Glu	Leu	Arg	His	Leu	Lys	Ile	Lys	Val	Glu	Glu		
				210					215					220			
ttg	gaa	aat	gaa	agg	aat	cag	tat	gaa	tgg	aag	cta	aag	gcc	act	aag	1083	
Leu	Glu	Asn	Glu	Arg	Asn	Gln	Tyr	Glu	Trp	Lys	Leu	Lys	Ala	Thr	Lys		
			225					230					235				
gct	gaa	gtc	gcc	cag	ctg	caa	gaa	cag	gtg	gcc	ctg	aaa	gat	gca	gaa	1131	
Ala	Glu	Val	Ala	Gln	Leu	Gln	Glu	Gln	Val	Ala	Leu	Lys	Asp	Ala	Glu		
	240					245						250					
att	gag	cgt	ctg	cac	agc	cag	ctc	tcc	cgg	aca	gca	gct	ctc	cac	agt	1179	
Ile	Glu	Arg	Leu	His	Ser	Gln	Leu	Ser	Arg	Thr	Ala	Ala	Leu	His	Ser		
	255					260					265						
gag	agt	cac	aca	gag	aga	gac	caa	gaa	att	caa	cgt	ctg	aaa	atg	ggg	1227	
Glu	Ser	His	Thr	Glu	Arg	Asp	Gln	Glu	Ile	Gln	Arg	Leu	Lys	Met	Gly		
270					275					280					285		
atg	gaa	act	ttg	ctg	ctt	gcc	aat	gaa	gat	aag	gac	cgt	cgg	ata	gag	1275	
Met	Glu	Thr	Leu	Leu	Leu	Ala	Asn	Glu	Asp	Lys	Asp	Arg	Arg	Ile	Glu		
				290					295					300			
gag	ctt	acg	ggg	ctg	tta	aac	cag	tac	cgg	aag	gta	aag	gag	att	gtg	1323	
Glu	Leu	Thr	Gly	Leu	Leu	Asn	Gln	Tyr	Arg	Lys	Val	Lys	Glu	Ile	Val		
			305					310					315				
atg	gtc	act	caa	ggg	cct	tcg	gag	aga	act	ctc	tca	atc	aat	gaa	gaa	1371	
Met	Val	Thr	Gln	Gly	Pro	Ser	Glu	Arg	Thr	Leu	Ser	Ile	Asn	Glu	Glu		
	320						325					330					
gaa	ccg	gag	gga	ggg	ttc	agc	aag	tgg	aac	gct	aca	aat	aag	gac	cct	1419	
Glu	Pro	Glu	Gly	Gly	Phe	Ser	Lys	Trp	Asn	Ala	Thr	Asn	Lys	Asp	Pro		
	335					340					345						
gaa	gaa	tta	ttt	aaa	caa	gag	atg	cct	cca	aga	tgt	agc	tct	cct	aca	1467	
Glu	Glu	Leu	Phe	Lys	Gln	Glu	Met	Pro	Pro	Arg	Cys	Ser	Ser	Pro	Thr		
350					355					360					365		
gtg	ggg	cca	cct	cca	ttg	cca	cag	aaa	tca	ctg	gaa	acc	agg	gct	cag	1515	
Val	Gly	Pro	Pro	Pro	Leu	Pro	Gln	Lys	Ser	Leu	Glu	Thr	Arg	Ala	Gln		
				370					375					380			
aaa	aag	ctc	tct	tgt	agt	cta	gaa	gac	ttg	aga	agt	gaa	tct	gtg	gat	1563	
Lys	Lys	Leu	Ser	Cys	Ser	Leu	Glu	Asp	Leu	Arg	Ser	Glu	Ser	Val	Asp		
			385					390					395				
aag	tgt	atg	gat	ggg	aac	cag	ccc	ttc	ccg	gtg	tta	gaa	ccc	aag	gac	1611	

Lys	Cys	Met	Asp	Gly	Asn	Gln	Pro	Phe	Pro	Val	Leu	Glu	Pro	Lys	Asp	
		400					405					410				
agc	cct	ttc	ttg	gcg	gag	cac	aaa	tat	ccc	act	tta	cct	ggg	aag	ctt	1659
Ser	Pro	Phe	Leu	Ala	Glu	His	Lys	Tyr	Pro	Thr	Leu	Pro	Gly	Lys	Leu	
	415					420					425					
tca	gga	gcc	acg	ccc	aat	gga	gag	gct	gcc	aaa	tct	cct	ccc	acc	atc	1707
Ser	Gly	Ala	Thr	Pro	Asn	Gly	Glu	Ala	Ala	Lys	Ser	Pro	Pro	Thr	Ile	
430					435					440					445	
tgc	cag	cct	gac	gcc	acg	ggg	agc	agc	ctg	ctg	agg	ctg	aga	gac	aca	1755
Cys	Gln	Pro	Asp	Ala	Thr	Gly	Ser	Ser	Leu	Leu	Arg	Leu	Arg	Asp	Thr	
				450					455					460		
gaa	agt	ggc	tgg	gac	gac	act	gct	gtg	gtc	aat	gac	ctc	tca	tcc	aca	1803
Glu	Ser	Gly	Trp	Asp	Asp	Thr	Ala	Val	Val	Asn	Asp	Leu	Ser	Ser	Thr	
			465				470					475				
tca	tcg	ggc	act	gaa	tca	ggg	cct	cag	tct	cct	ctg	aca	cca	gat	ggg	1851
Ser	Ser	Gly	Thr	Glu	Ser	Gly	Pro	Gln	Ser	Pro	Leu	Thr	Pro	Asp	Gly	
		480					485					490				
aaa	cgg	aat	ccc	aaa	ggc	att	aag	aag	ttc	tgg	gga	aaa	atc	cga	aga	1899
Lys	Arg	Asn	Pro	Lys	Gly	Ile	Lys	Lys	Phe	Trp	Gly	Lys	Ile	Arg	Arg	
	495					500					505					
act	cag	tca	gga	aat	ttc	tac	act	gac	acg	ctg	ggg	atg	gca	gag	ttt	1947
Thr	Gln	Ser	Gly	Asn	Phe	Tyr	Thr	Asp	Thr	Leu	Gly	Met	Ala	Glu	Phe	
510					515					520					525	
cga	cga	ggg	ggg	ctc	cgg	gca	acc	gca	ggg	cca	aga	ctc	tct	agg	acc	1995
Arg	Arg	Gly	Gly	Leu	Arg	Ala	Thr	Ala	Gly	Pro	Arg	Leu	Ser	Arg	Thr	
				530					535					540		
agg	gac	tcc	aag	gga	cag	aaa	agt	gac	gcc	aat	gcc	ccc	ttt	gcc	cag	2043
Arg	Asp	Ser	Lys	Gly	Gln	Lys	Ser	Asp	Ala	Asn	Ala	Pro	Phe	Ala	Gln	
			545					550					555			
tgg	agc	aca	gag	cgt	gtg	tgt	gca	tgg	ctg	gag	gac	ttt	ggc	ctg	gct	2091
Trp	Ser	Thr	Glu	Arg	Val	Cys	Ala	Trp	Leu	Glu	Asp	Phe	Gly	Leu	Ala	
		560					565					570				
cag	tat	gtg	atc	ttt	gcc	agg	cag	tgg	gta	tct	tct	ggc	cac	acc	tta	2139
Gln	Tyr	Val	Ile	Phe	Ala	Arg	Gln	Trp	Val	Ser	Ser	Gly	His	Thr	Leu	
	575					580					585					
ttg	aca	gcc	acc	cct	cag	gac	atg	gaa	aag	gag	cta	gga	att	aag	cac	2187
Leu	Thr	Ala	Thr	Pro	Gln	Asp	Met	Glu	Lys	Glu	Leu	Gly	Ile	Lys	His	
590					595					600					605	
cca	ctc	cac	agg	aag	aag	ctt	gtt	tta	gca	gtg	aaa	gcc	atc	aac	acc	2235
Pro	Leu	His	Arg	Lys	Lys	Leu	Val	Leu	Ala	Val	Lys	Ala	Ile	Asn	Thr	
				610					615					620		
aaa	cag	gag	gag	aag	tct	gca	ctg	cta	gac	cac	att	tgg	gtg	aca	agg	2283
Lys	Gln	Glu	Glu	Lys	Ser	Ala	Leu	Leu	Asp	His	Ile	Trp	Val	Thr	Arg	
			625					630					635			
tgg	ctt	gat	gat	att	ggc	tta	ccc	cag	tac	aaa	gac	cag	ttt	cat	gaa	2331

Trp	Leu	Asp	Asp	Ile	Gly	Leu	Pro	Gln	Tyr	Lys	Asp	Gln	Phe	His	Glu		
		640					645					650					
tct	aga	gtt	gac	aga	cga	atg	ctg	caa	tac	cta	act	gtg	aac	gat	tta	2379	
Ser	Arg	Val	Asp	Arg	Arg	Met	Leu	Gln	Tyr	Leu	Thr	Val	Asn	Asp	Leu		
	655					660					665						
ctc	ttc	tta	aaa	gtc	acc	agc	caa	cta	cat	cat	ctc	agc	atc	aaa	tgt	2427	
Leu	Phe	Leu	Lys	Val	Thr	Ser	Gln	Leu	His	His	Leu	Ser	Ile	Lys	Cys		
670					675					680					685		
gcc	att	cac	gtg	ctg	cat	gtc	aac	aag	ttc	aac	ccc	cac	tgc	ctg	cac	2475	
Ala	Ile	His	Val	Leu	His	Val	Asn	Lys	Phe	Asn	Pro	His	Cys	Leu	His		
				690					695					700			
cgg	cgg	cca	gct	gat	gag	agt	aac	ctt	tct	cct	tca	gaa	gtt	gta	cag	2523	
Arg	Arg	Pro	Ala	Asp	Glu	Ser	Asn	Leu	Ser	Pro	Ser	Glu	Val	Val	Gln		
		705						710					715				
tgg	tcc	aac	cac	agg	gtg	atg	gag	tgg	tta	cga	tct	gtg	gac	ctg	gca	2571	
Trp	Ser	Asn	His	Arg	Val	Met	Glu	Trp	Leu	Arg	Ser	Val	Asp	Leu	Ala		
	720						725					730					
gag	tat	gca	ccc	aat	ctt	cga	ggg	agt	gga	gtc	cat	gga	ggc	ctc	att	2619	
Glu	Tyr	Ala	Pro	Asn	Leu	Arg	Gly	Ser	Gly	Val	His	Gly	Gly	Leu	Ile		
	735					740					745						
atc	ctg	gag	cca	cgc	ttc	act	ggg	gac	acc	ctg	gct	atg	ctt	ctc	aac	2667	
Ile	Leu	Glu	Pro	Arg	Phe	Thr	Gly	Asp	Thr	Leu	Ala	Met	Leu	Leu	Asn		
750					755					760					765		
atc	ccc	cca	caa	aag	acg	ctc	ctc	agg	cgc	cac	ctg	acc	acc	aag	ttc	2715	
Ile	Pro	Pro	Gln	Lys	Thr	Leu	Leu	Arg	Arg	His	Leu	Thr	Thr	Lys	Phe		
			770					775						780			
aat	gcc	ttg	att	ggc	ccg	gag	gct	gaa	cag	gag	aag	cga	gag	aaa	atg	2763	
Asn	Ala	Leu	Ile	Gly	Pro	Glu	Ala	Glu	Gln	Glu	Lys	Arg	Glu	Lys	Met		
		785					790						795				
gcc	tca	cca	gct	tac	aca	cca	ctg	acc	acc	aca	gcc	aaa	gtc	cgg	cca	2811	
Ala	Ser	Pro	Ala	Tyr	Thr	Pro	Leu	Thr	Thr	Thr	Ala	Lys	Val	Arg	Pro		
		800					805					810					
agg	aaa	cta	gga	ttt	tca	cac	ttc	gga	aac	ata	aga	aaa	aag	aag	ttc	2859	
Arg	Lys	Leu	Gly	Phe	Ser	His	Phe	Gly	Asn	Ile	Arg	Lys	Lys	Lys	Phe		
	815					820					825						
gat	gaa	tcg	acg	gac	tac	att	tgc	cca	atg	gag	ccc	agt	gac	ggc	gtc	2907	
Asp	Glu	Ser	Thr	Asp	Tyr	Ile	Cys	Pro	Met	Glu	Pro	Ser	Asp	Gly	Val		
830					835					840					845		
agt	gat	agt	cac	agg	gtc	tac	agt	ggc	tac	cgg	ggc	ctc	agc	ccc	ctt	2955	
Ser	Asp	Ser	His	Arg	Val	Tyr	Ser	Gly	Tyr	Arg	Gly	Leu	Ser	Pro	Leu		
				850				855						860			
gat	gcc	cct	gaa	ctg	gat	ggg	ctg	gac	cag	gtg	gga	cag	att	agc	tga	3003	
Asp	Ala	Pro	Glu	Leu	Asp	Gly	Leu	Asp	Gln	Val	Gly	Gln	Ile	Ser			
		865					870					875					
tgcccttgtc	acctgccctc	tgtgcaccct	gagagctcac	agtaacactg	tgtgtgtcac											3063	

catataactg cacctcaccc ccgcacgtgt gcatgactcg cagagaatat tccagcaatt 3123
gtgtaccctt gggccagtct ctttgaaccc tgagggtggc caggatctgg agctgcatct 3183
ctaagggggc aggctttggg gaccattgcc aaaggtggac tcaggaggaa agacacttaa 3243
agacactttt acatgtctag taattcttga tgttcatctt cagcaccagt ggaaacacat 3303
gaacttcgat gcaggtccag agaccatgga cactcccacg aggctcagct ctcaggcacc 3363
ccctacactt cagttgaggg aaaagctcaa gtgccttagg cccgtggacc acagtcttgg 3423
ctgagatcaa agggatgagc aacagggact tctgccacag tgacaatgga attgtgttgt 3483
gccttacttc agaggtggtc tcttctttct tgtaataaaa gcaatattta tgcggaaagc 3543

<210> 46
<211> 876
<212> PRT
<213> human

<400> 46

Met Ala Ser Asp Ala Ser His Ala Leu Glu Ala Ala Leu Glu Gln Met
1 5 10 15

Asp Gly Ile Ile Ala Gly Thr Lys Thr Gly Ala Asp Leu Ser Asp Gly
20 25 30

Thr Cys Glu Pro Gly Leu Ala Ser Pro Ala Ser Tyr Met Asn Pro Phe
35 40 45

Pro Val Leu His Leu Ile Glu Asp Leu Arg Leu Ala Leu Glu Met Leu
50 55 60

Glu Leu Pro Gln Glu Arg Ala Ala Leu Leu Ser Gln Ile Pro Gly Pro
65 70 75 80

Thr Ala Ala Tyr Ile Lys Glu Trp Phe Glu Glu Ser Leu Ser Gln Val
85 90 95

Asn His His Ser Ala Ala Ser Asn Glu Thr Tyr Gln Glu Arg Leu Ala
100 105 110

Arg Leu Glu Gly Asp Lys Glu Ser Leu Ile Leu Gln Val Ser Val Leu
115 120 125

Thr Asp Gln Val Glu Ala Gln Gly Glu Lys Ile Arg Asp Leu Glu Val
130 135 140

Cys	Leu	Glu	Gly	His	Gln	Val	Lys	Leu	Asn	Ala	Ala	Glu	Glu	Met	Leu	145	150	155	160
Gln	Gln	Glu	Leu	Leu	Ser	Arg	Thr	Ser	Leu	Glu	Thr	Gln	Lys	Leu	Asp	165	170	175	
Leu	Met	Thr	Glu	Val	Ser	Glu	Leu	Lys	Leu	Lys	Leu	Val	Gly	Met	Glu	180	185	190	
Lys	Glu	Gln	Arg	Glu	Gln	Glu	Glu	Lys	Gln	Arg	Lys	Ala	Glu	Glu	Leu	195	200	205	
Leu	Gln	Glu	Leu	Arg	His	Leu	Lys	Ile	Lys	Val	Glu	Glu	Leu	Glu	Asn	210	215	220	
Glu	Arg	Asn	Gln	Tyr	Glu	Trp	Lys	Leu	Lys	Ala	Thr	Lys	Ala	Glu	Val	225	230	235	240
Ala	Gln	Leu	Gln	Glu	Gln	Val	Ala	Leu	Lys	Asp	Ala	Glu	Ile	Glu	Arg	245	250	255	
Leu	His	Ser	Gln	Leu	Ser	Arg	Thr	Ala	Ala	Leu	His	Ser	Glu	Ser	His	260	265	270	
Thr	Glu	Arg	Asp	Gln	Glu	Ile	Gln	Arg	Leu	Lys	Met	Gly	Met	Glu	Thr	275	280	285	
Leu	Leu	Leu	Ala	Asn	Glu	Asp	Lys	Asp	Arg	Arg	Ile	Glu	Glu	Leu	Thr	290	295	300	
Gly	Leu	Leu	Asn	Gln	Tyr	Arg	Lys	Val	Lys	Glu	Ile	Val	Met	Val	Thr	305	310	315	320
Gln	Gly	Pro	Ser	Glu	Arg	Thr	Leu	Ser	Ile	Asn	Glu	Glu	Glu	Pro	Glu	325	330	335	
Gly	Gly	Phe	Ser	Lys	Trp	Asn	Ala	Thr	Asn	Lys	Asp	Pro	Glu	Glu	Leu	340	345	350	
Phe	Lys	Gln	Glu	Met	Pro	Pro	Arg	Cys	Ser	Ser	Pro	Thr	Val	Gly	Pro	355	360	365	
Pro	Pro	Leu	Pro	Gln	Lys	Ser	Leu	Glu	Thr	Arg	Ala	Gln	Lys	Lys	Leu	370	375	380	

Ser Cys Ser Leu Glu Asp Leu Arg Ser Glu Ser Val Asp Lys Cys Met
 385 390 395 400

Asp Gly Asn Gln Pro Phe Pro Val Leu Glu Pro Lys Asp Ser Pro Phe
 405 410 415

Leu Ala Glu His Lys Tyr Pro Thr Leu Pro Gly Lys Leu Ser Gly Ala
 420 425 430

Thr Pro Asn Gly Glu Ala Ala Lys Ser Pro Pro Thr Ile Cys Gln Pro
 435 440 445

Asp Ala Thr Gly Ser Ser Leu Leu Arg Leu Arg Asp Thr Glu Ser Gly
 450 455 460

Trp Asp Asp Thr Ala Val Val Asn Asp Leu Ser Ser Thr Ser Ser Gly
 465 470 475 480

Thr Glu Ser Gly Pro Gln Ser Pro Leu Thr Pro Asp Gly Lys Arg Asn
 485 490 495

Pro Lys Gly Ile Lys Lys Phe Trp Gly Lys Ile Arg Arg Thr Gln Ser
 500 505 510

Gly Asn Phe Tyr Thr Asp Thr Leu Gly Met Ala Glu Phe Arg Arg Gly
 515 520 525

Gly Leu Arg Ala Thr Ala Gly Pro Arg Leu Ser Arg Thr Arg Asp Ser
 530 535 540

Lys Gly Gln Lys Ser Asp Ala Asn Ala Pro Phe Ala Gln Trp Ser Thr
 545 550 555 560

Glu Arg Val Cys Ala Trp Leu Glu Asp Phe Gly Leu Ala Gln Tyr Val
 565 570 575

Ile Phe Ala Arg Gln Trp Val Ser Ser Gly His Thr Leu Leu Thr Ala
 580 585 590

Thr Pro Gln Asp Met Glu Lys Glu Leu Gly Ile Lys His Pro Leu His
 595 600 605

Arg Lys Lys Leu Val Leu Ala Val Lys Ala Ile Asn Thr Lys Gln Glu
 610 615 620

Glu Lys Ser Ala Leu Leu Asp His Ile Trp Val Thr Arg Trp Leu Asp
625 630 635 640

Asp Ile Gly Leu Pro Gln Tyr Lys Asp Gln Phe His Glu Ser Arg Val
645 650 655

Asp Arg Arg Met Leu Gln Tyr Leu Thr Val Asn Asp Leu Leu Phe Leu
660 665 670

Lys Val Thr Ser Gln Leu His His Leu Ser Ile Lys Cys Ala Ile His
675 680 685

Val Leu His Val Asn Lys Phe Asn Pro His Cys Leu His Arg Arg Pro
690 695 700

Ala Asp Glu Ser Asn Leu Ser Pro Ser Glu Val Val Gln Trp Ser Asn
705 710 715 720

His Arg Val Met Glu Trp Leu Arg Ser Val Asp Leu Ala Glu Tyr Ala
725 730 735

Pro Asn Leu Arg Gly Ser Gly Val His Gly Gly Leu Ile Ile Leu Glu
740 745 750

Pro Arg Phe Thr Gly Asp Thr Leu Ala Met Leu Leu Asn Ile Pro Pro
755 760 765

Gln Lys Thr Leu Leu Arg Arg His Leu Thr Thr Lys Phe Asn Ala Leu
770 775 780

Ile Gly Pro Glu Ala Glu Gln Glu Lys Arg Glu Lys Met Ala Ser Pro
785 790 795 800

Ala Tyr Thr Pro Leu Thr Thr Thr Ala Lys Val Arg Pro Arg Lys Leu
805 810 815

Gly Phe Ser His Phe Gly Asn Ile Arg Lys Lys Lys Phe Asp Glu Ser
820 825 830

Thr Asp Tyr Ile Cys Pro Met Glu Pro Ser Asp Gly Val Ser Asp Ser
835 840 845

His Arg Val Tyr Ser Gly Tyr Arg Gly Leu Ser Pro Leu Asp Ala Pro
850 855 860

Glu Leu Asp Gly Leu Asp Gln Val Gly Gln Ile Ser
 865 870 875

<210> 47
 <211> 2819
 <212> DNA
 <213> human

<220>
 <221> CDS
 <222> (77)..(1180)

<400> 47
 ctgggcccag ctccccgag aggtggctgg atcctctggg ctgctcggtc gatgcctgtg 60
 ccactgacgt ccaggc atg agg tgg ttc ctg ccc tgg acg ctg gca gca gtg 112
 Met Arg Trp Phe Leu Pro Trp Thr Leu Ala Ala Val
 1 5 10
 aca gca gca gcc gcc agc acc gtc ctg gcc acg gcc ctc tct cca gcc 160
 Thr Ala Ala Ala Ala Ser Thr Val Leu Ala Thr Ala Leu Ser Pro Ala
 15 20 25
 cct acg acc atg gac ttt acc cca gct cca ctg gag gac acc tcc tca 208
 Pro Thr Thr Met Asp Phe Thr Pro Ala Pro Leu Glu Asp Thr Ser Ser
 30 35 40
 cgc ccc caa ttc tgc aag tgg cca tgt gag tgc ccg cca tcc cca ccc 256
 Arg Pro Gln Phe Cys Lys Trp Pro Cys Glu Cys Pro Pro Ser Pro Pro
 45 50 55 60
 cgc tgc ccg ctg ggg gtc agc ctc atc aca gat ggc tgt gag tgc tgt 304
 Arg Cys Pro Leu Gly Val Ser Leu Ile Thr Asp Gly Cys Glu Cys Cys
 65 70 75
 aag atg tgc gct cag cag ctt ggg gac aac tgc acg gag gct gcc atc 352
 Lys Met Cys Ala Gln Gln Leu Gly Asp Asn Cys Thr Glu Ala Ala Ile
 80 85 90
 tgt gac ccc cac cgg ggc ctc tac tgt gac tac agc ggg gac cgc ccg 400
 Cys Asp Pro His Arg Gly Leu Tyr Cys Asp Tyr Ser Gly Asp Arg Pro
 95 100 105
 agg tac gca ata gga gtg tgt gca cag gtg gtc ggt gtg ggc tgc gtc 448
 Arg Tyr Ala Ile Gly Val Cys Ala Gln Val Val Gly Val Gly Cys Val
 110 115 120
 ctg gat ggg gtg cgc tac aac aac ggc cag tcc ttc cag cct aac tgc 496
 Leu Asp Gly Val Arg Tyr Asn Asn Gly Gln Ser Phe Gln Pro Asn Cys
 125 130 135 140
 aag tac aac tgc acg tgc atc gac ggc gcg gtg ggc tgc aca cca ctg 544
 Lys Tyr Asn Cys Thr Cys Ile Asp Gly Ala Val Gly Cys Thr Pro Leu
 145 150 155
 tgc ctc cga gtg cgc ccc ccg cgt ctc tgg tgc ccc cac ccg cgg cgc 592
 Cys Leu Arg Val Arg Pro Pro Arg Leu Trp Cys Pro His Pro Arg Arg

160	165	170	
gtg agc ata cct ggc cac tgc tgt gag cag tgg gta tgt gag gac gac Val Ser Ile Pro Gly His Cys Cys Glu Gln Trp Val Cys Glu Asp Asp 175 180 185			640
gcc aag agg cca cgc aag acc gca ccc cgt gac aca gga gcc ttc gat Ala Lys Arg Pro Arg Lys Thr Ala Pro Arg Asp Thr Gly Ala Phe Asp 190 195 200			688
gct gtg ggt gag gtg gag gca tgg cac agg aac tgc ata gcc tac aca Ala Val Gly Glu Val Glu Ala Trp His Arg Asn Cys Ile Ala Tyr Thr 205 210 215 220			736
agc ccc tgg agc cct tgc tcc acc agc tgc ggc ctg ggg gtc tcc act Ser Pro Trp Ser Pro Cys Ser Thr Ser Cys Gly Leu Gly Val Ser Thr 225 230 235			784
cgg atc tcc aat gtt aac gcc cag tgc tgg cct gag caa gag agc cgc Arg Ile Ser Asn Val Asn Ala Gln Cys Trp Pro Glu Gln Glu Ser Arg 240 245 250			832
ctc tgc aac ttg cgg cca tgc gat gtg gac atc cat aca ctc att aag Leu Cys Asn Leu Arg Pro Cys Asp Val Asp Ile His Thr Leu Ile Lys 255 260 265			880
gca ggg aag aag tgt ctg gct gtg tac cag cca gag gca tcc atg aac Ala Gly Lys Lys Cys Leu Ala Val Tyr Gln Pro Glu Ala Ser Met Asn 270 275 280			928
ttc aca ctt gcg ggc tgc atc agc aca cgc tcc tat caa ccc aag tac Phe Thr Leu Ala Gly Cys Ile Ser Thr Arg Ser Tyr Gln Pro Lys Tyr 285 290 295 300			976
tgt gga gtt tgc atg gac aat agg tgc tgc atc ccc tac aag tct aag Cys Gly Val Cys Met Asp Asn Arg Cys Cys Ile Pro Tyr Lys Ser Lys 305 310 315			1024
act atc gac gtg tcc ttc cag tgt cct gat ggg ctt ggc ttc tcc cgc Thr Ile Asp Val Ser Phe Gln Cys Pro Asp Gly Leu Gly Phe Ser Arg 320 325 330			1072
cag gtc cta tgg att aat gcc tgc ttc tgt aac ctg agc tgt agg aat Gln Val Leu Trp Ile Asn Ala Cys Phe Cys Asn Leu Ser Cys Arg Asn 335 340 345			1120
ccc aat gac atc ttt gct gac ttg gaa tcc tac cct gac ttc tca gaa Pro Asn Asp Ile Phe Ala Asp Leu Glu Ser Tyr Pro Asp Phe Ser Glu 350 355 360			1168
att gcc aac tag gcaggcacia atcttgggtc ttggggacta acccaatgcc Ile Ala Asn 365			1220
tgtgaagcag tcagccctta tggccaataa cttttcacca atgagcctta gttaccctga			1280
tctggaccct tggcctccat ttctgtctct aaccattcaa atgacgcctg atgggtgctgc			1340
tcaggcccat gctatgagtt ttctccttga tatcattcag catctactct aaagaaaaat			1400

```

gacctgtctct agctgttctg gactacaccc aagcctgata cagcctttcc aagtcactag 1460
aagtcctgct ggatcttgcc taaatcccaa gaaatggaat caggtagact tttaatatca 1520
ctaatttctt ctttagatgc caaaccacaa gactctttgg gtccattcag atgaatagat 1580
ggaatttggg acaatagaat aatctattat ttggagcctg ccaagaggta ctgtaatggg 1640
taattctgac gtcagcgcac caaaactatc ctgattccaa atatgtatgc acctcaaggt 1700
catcaaacat ttgccaagtg agttgaatag ttgcttaatt ttgattttta atggaaagtt 1760
gtatccatta acctgggcat tgttgagggt aagtttctct tcacccctac actgtgaagg 1820
gtacagatta ggtttgtccc agtcagaaat aaaatttgat aaacattcct gttgatggga 1880
aaagccccc a gttaatactc cagagacagg gaaagggtcag cccgtttcag aaggaccaat 1940
tgactctcac actgaatcag ctgctgactg gcagggcctt gggcagttgg ccaggctctt 2000
ccttgaatct tctcccttgt cctgcttggg gttcatagga attggtaagg cctctggact 2060
ggcctgtctg gccctgaga gtggtgccct ggaacactcc tctactctta cagagccttg 2120
agagaccag ctgcagacca tgccagaccc actgaaatga ccaagacagg ttcaggtagg 2180
gggtgtgggtc aaaccaagaa gtgggtgccc ttggtagcag cctgggggtga cctctagagc 2240
tggaggctgt gggactccag gggccccgt gttcaggaca catctattgc agagactcat 2300
ttcacagcct ttcgttctgc tgaccaaagt gccagttttc tggtaggaag atggagggtt 2360
accggttgt tagaaacaga aatagactta ataaagggtt aaagctgaag aggttgaagc 2420
taaaaggaaa aggttgttgt taatgaatat caggctatta tttattgtat taggaaaata 2480
taatatttac tgtagaatt cttttattta gggccttttc tgtgccagac attgctctca 2540
gtgctttgca tgtattagct cactgaatct tcacgacaat gttgagaagt tccattatt 2600
atctctgttc ttacaaatgt gaaacggaag ctcatagagg tgagaaaact caaccagagt 2660
caccagttg gtgactggga aagttaggat tcagatcgaa attggactgt cttataacc 2720
catattttcc cctgttttt agagcttcca aatgtgtcag aataggaaaa cattgcaata 2780
aatggcttga ttttttaaaa aaaaaaaaaa aaaaaaaaaa 2819

```

```

<210> 48
<211> 367
<212> PRT
<213> human

```

```

<400> 48

```

```

Met Arg Trp Phe Leu Pro Trp Thr Leu Ala Ala Val Thr Ala Ala Ala
1           5           10          15

```


Ala Ser Thr Val Leu Ala Thr Ala Leu Ser Pro Ala Pro Thr Thr Met
 20 25 30

Asp Phe Thr Pro Ala Pro Leu Glu Asp Thr Ser Ser Arg Pro Gln Phe
 35 40 45

Cys Lys Trp Pro Cys Glu Cys Pro Pro Ser Pro Pro Arg Cys Pro Leu
 50 55 60

Gly Val Ser Leu Ile Thr Asp Gly Cys Glu Cys Cys Lys Met Cys Ala
 65 70 75 80

Gln Gln Leu Gly Asp Asn Cys Thr Glu Ala Ala Ile Cys Asp Pro His
 85 90 95

Arg Gly Leu Tyr Cys Asp Tyr Ser Gly Asp Arg Pro Arg Tyr Ala Ile
 100 105 110

Gly Val Cys Ala Gln Val Val Gly Val Gly Cys Val Leu Asp Gly Val
 115 120 125

Arg Tyr Asn Asn Gly Gln Ser Phe Gln Pro Asn Cys Lys Tyr Asn Cys
 130 135 140

Thr Cys Ile Asp Gly Ala Val Gly Cys Thr Pro Leu Cys Leu Arg Val
 145 150 155 160

Arg Pro Pro Arg Leu Trp Cys Pro His Pro Arg Arg Val Ser Ile Pro
 165 170 175

Gly His Cys Cys Glu Gln Trp Val Cys Glu Asp Asp Ala Lys Arg Pro
 180 185 190

Arg Lys Thr Ala Pro Arg Asp Thr Gly Ala Phe Asp Ala Val Gly Glu
 195 200 205

Val Glu Ala Trp His Arg Asn Cys Ile Ala Tyr Thr Ser Pro Trp Ser
 210 215 220

Pro Cys Ser Thr Ser Cys Gly Leu Gly Val Ser Thr Arg Ile Ser Asn
 225 230 235 240

Val Asn Ala Gln Cys Trp Pro Glu Gln Glu Ser Arg Leu Cys Asn Leu
 245 250 255

Arg Pro Cys Asp Val Asp Ile His Thr Leu Ile Lys Ala Gly Lys Lys
 260 265 270

Cys Leu Ala Val Tyr Gln Pro Glu Ala Ser Met Asn Phe Thr Leu Ala
 275 280 285

Gly Cys Ile Ser Thr Arg Ser Tyr Gln Pro Lys Tyr Cys Gly Val Cys
 290 295 300

Met Asp Asn Arg Cys Cys Ile Pro Tyr Lys Ser Lys Thr Ile Asp Val
 305 310 315 320

Ser Phe Gln Cys Pro Asp Gly Leu Gly Phe Ser Arg Gln Val Leu Trp
 325 330 335

Ile Asn Ala Cys Phe Cys Asn Leu Ser Cys Arg Asn Pro Asn Asp Ile
 340 345 350

Phe Ala Asp Leu Glu Ser Tyr Pro Asp Phe Ser Glu Ile Ala Asn
 355 360 365

<210> 49
 <211> 1768
 <212> DNA
 <213> human

<220>
 <221> CDS
 <222> (356)..(868)

<400> 49
 ggcacgagggc tgctgtctgc ggaggaaact gcatcgacgg acggccgccc agctacggga 60
 ggacctggag tggcactggg cgcccgcagg accatccccg ggaccgcct gccctcggc 120
 gccccgcccc gccgggccgc tccccgtcgg gttccccagc cacagcctta cctacgggct 180
 cctgactccg caaggcttcc agaagatgct cgaaccaccg gccggggcct cggggcagca 240
 gtgagggagg cgtccagccc ccactcagc tcttctctc ctgtgccagg ggctccccgg 300
 gggatgagca tgggtggtttt ccctcggagc cccctggctc gggacgtctg agaag atg 358
 Met
 1
 ccg gtc atg agg ctg ttc cct tgc ttc ctg cag ctc ctg gcc ggg ctg 406
 Pro Val Met Arg Leu Phe Pro Cys Phe Leu Gln Leu Leu Ala Gly Leu
 5 10 15
 gcg ctg cct gct gtg ccc ccc cag cag tgg gcc ttg tct gct ggg aac 454
 Ala Leu Pro Ala Val Pro Pro Gln Gln Trp Ala Leu Ser Ala Gly Asn
 20 25 30

ggc tgc tca gag gtg gaa gtg gta ccc ttc cag gaa gtg tgg ggc cgc	502
Gly Ser Ser Glu Val Glu Val Val Pro Phe Gln Glu Val Trp Gly Arg	
35 40 45	
agc tac tgc cgg gcg ctg gag agg ctg gtg gac gtc gtg tcc gag tac	550
Ser Tyr Cys Arg Ala Leu Glu Arg Leu Val Asp Val Val Ser Glu Tyr	
50 55 60 65	
ccc agc gag gtg gag cac atg ttc agc cca tcc tgt gtc tcc ctg ctg	598
Pro Ser Glu Val Glu His Met Phe Ser Pro Ser Cys Val Ser Leu Leu	
70 75 80	
cgc tgc acc ggc tgc tgc ggc gat gag aat ctg cac tgt gtg ccg gtg	646
Arg Cys Thr Gly Cys Cys Gly Asp Glu Asn Leu His Cys Val Pro Val	
85 90 95	
gag acg gcc aat gtc acc atg cag ctc cta aag atc cgt tct ggg gac	694
Glu Thr Ala Asn Val Thr Met Gln Leu Leu Lys Ile Arg Ser Gly Asp	
100 105 110	
cgg ccc tcc tac gtg gag ctg acg ttc tct cag cac gtt cgc tgc gaa	742
Arg Pro Ser Tyr Val Glu Leu Thr Phe Ser Gln His Val Arg Cys Glu	
115 120 125	
tgc cgg cct ctg cgg gag aag atg aag ccg gaa agg agg aga ccc aag	790
Cys Arg Pro Leu Arg Glu Lys Met Lys Pro Glu Arg Arg Arg Pro Lys	
130 135 140 145	
ggc agg ggg aag agg agg aga gag aag cag aga ccc aca gac tgc cac	838
Gly Arg Gly Lys Arg Arg Arg Glu Lys Gln Arg Pro Thr Asp Cys His	
150 155 160	
ctg tgc ggc gat gct gtt ccc cgg agg taa cccacccctt ggaggagaga	888
Leu Cys Gly Asp Ala Val Pro Arg Arg	
165 170	
gaccccgcac ccggctcgtg tatttattac cgtcacactc ttcagtgact cctgctggta	948
cctgccctct atttattagc caactgtttc cctgctgaat gcctcgctcc cttcaagacg	1008
aggggcaggg aaggacagga ccctcaggaa ttcagtgcct tcaacaacgt gagagaaaga	1068
gagaagccag ccacagaccc ctgggagctt ccgctttgaa agaagcaaga cacgtggcct	1128
cgtgaggggc aagctaggcc ccagaggccc tggaggtctc caggggcctg cagaaggaaa	1188
gaagggggcc ctgctacctg ttcttgggcc tcaggctctg cacagtcaag cagcccttgc	1248
tttcggagct cctgtccaaa agtagggatg cggatcctgc tggggccgcc acggcctggc	1308
tggtgggaag gccggcagcg ggcggagggg atccagccac ttccccctct tcttctgaag	1368
atcagaacat tcagctctgg agaacagtgg ttgcctgggg gcttttgcca ctcttgtcc	1428
cccgtgatct cccctcacac tttgccattt gcttgtactg ggacattgtt ctttccggcc	1488
aagggtgccac caccctgccc ccctaagag acacatacag agtgggcccc gggctggaga	1548
aagagctgcc tggatgagaa acagctcagc cagtggggat gaggtcacca ggggaggagc	1608

ctgtgcggtcc cagctgaagg cagtggcagg ggagcaggtt cccaagggc cctggcaccc 1668
ccacaagctg tccctgcagg gccatctgac tgccaagcca gattctcttg aataaagtat 1728
tctagtgtgg aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1768

<210> 50
<211> 170
<212> PRT
<213> human

<400> 50

Met Pro Val Met Arg Leu Phe Pro Cys Phe Leu Gln Leu Leu Ala Gly
1 5 10 15

Leu Ala Leu Pro Ala Val Pro Pro Gln Gln Trp Ala Leu Ser Ala Gly
20 25 30

Asn Gly Ser Ser Glu Val Glu Val Val Pro Phe Gln Glu Val Trp Gly
35 40 45

Arg Ser Tyr Cys Arg Ala Leu Glu Arg Leu Val Asp Val Val Ser Glu
50 55 60

Tyr Pro Ser Glu Val Glu His Met Phe Ser Pro Ser Cys Val Ser Leu
65 70 75 80

Leu Arg Cys Thr Gly Cys Cys Gly Asp Glu Asn Leu His Cys Val Pro
85 90 95

Val Glu Thr Ala Asn Val Thr Met Gln Leu Leu Lys Ile Arg Ser Gly
100 105 110

Asp Arg Pro Ser Tyr Val Glu Leu Thr Phe Ser Gln His Val Arg Cys
115 120 125

Glu Cys Arg Pro Leu Arg Glu Lys Met Lys Pro Glu Arg Arg Arg Pro
130 135 140

Lys Gly Arg Gly Lys Arg Arg Arg Glu Lys Gln Arg Pro Thr Asp Cys
145 150 155 160

His Leu Cys Gly Asp Ala Val Pro Arg Arg
165 170

<210> 51

<211> 3874
 <212> DNA
 <213> human

<220>
 <221> CDS
 <222> (1)..(1902)

```

<400> 51
atg gct cac cta aag cga cta gta aaa tta cac att aaa aga cat tac      48
Met Ala His Leu Lys Arg Leu Val Lys Leu His Ile Lys Arg His Tyr
1                               5                               10          15

cat aaa aag ttc tgg aag ctt ggt gca gta att ttt ttc ttt ata ata      96
His Lys Lys Phe Trp Lys Leu Gly Ala Val Ile Phe Phe Phe Ile Ile
                20                               25          30

gtt ttg gtt tta atg caa aga gaa gta agt gtt caa tat tcc aaa gag      144
Val Leu Val Leu Met Gln Arg Glu Val Ser Val Gln Tyr Ser Lys Glu
                35                               40          45

gaa tca agg atg gaa agg aac atg aaa aac aaa aac aag atg ttg gat      192
Glu Ser Arg Met Glu Arg Asn Met Lys Asn Lys Asn Lys Met Leu Asp
                50                               55          60

tta atg cta gaa gct gta aac aat att aag gat gcc atg cca aaa atg      240
Leu Met Leu Glu Ala Val Asn Asn Ile Lys Asp Ala Met Pro Lys Met
65                               70          75          80

caa ata gga gca cct gtc agg caa aac att gat gct ggt gag aga cct      288
Gln Ile Gly Ala Pro Val Arg Gln Asn Ile Asp Ala Gly Glu Arg Pro
                85                               90          95

tgt ttg caa gga tat tat aca gca gca gaa ttg aag cct gtc ctt gac      336
Cys Leu Gln Gly Tyr Tyr Thr Ala Ala Glu Leu Lys Pro Val Leu Asp
                100                              105          110

cgt cca cct cag gat tca aat gca cct ggt gct tct ggt aaa gca ttc      384
Arg Pro Pro Gln Asp Ser Asn Ala Pro Gly Ala Ser Gly Lys Ala Phe
                115                              120          125

aag aca acc aat tta agt gtt gaa gag caa aag gaa aag gaa cgt ggg      432
Lys Thr Thr Asn Leu Ser Val Glu Glu Gln Lys Glu Lys Glu Arg Gly
                130                              135          140

gaa gct aaa cac tgc ttt aat gct ttc gca agt gac agg att tct ttg      480
Glu Ala Lys His Cys Phe Asn Ala Phe Ala Ser Asp Arg Ile Ser Leu
145                              150          155          160

cac cga gat ctt gga cca gac act cga cct cct gaa tgt att gaa caa      528
His Arg Asp Leu Gly Pro Asp Thr Arg Pro Pro Glu Cys Ile Glu Gln
                165                              170          175

aaa ttt aag cgc tgc cct ccc ctg ccc acc acc agt gtc ata ata gtt      576
Lys Phe Lys Arg Cys Pro Pro Leu Pro Thr Thr Ser Val Ile Ile Val
                180                              185          190

ttt cat aat gaa gcg tgg tcc acg ttg ctt aga act gtc cac agt gtg      624
Phe His Asn Glu Ala Trp Ser Thr Leu Leu Arg Thr Val His Ser Val

```

195	200	205	
ctc tat tct tca cct gca ata ctg ctg aag gaa atc att ttg gtg gat Leu Tyr Ser Ser Pro Ala Ile Leu Leu Lys Glu Ile Ile Leu Val Asp 210 215 220			672
gat gct agt gta gat gag tac tta cat gat aaa cta gat gaa tat gta Asp Ala Ser Val Asp Glu Tyr Leu His Asp Lys Leu Asp Glu Tyr Val 225 230 235 240			720
aaa caa ttt tct ata gta aaa ata gtc aga caa aga gaa aga aaa ggt Lys Gln Phe Ser Ile Val Lys Ile Val Arg Gln Arg Glu Arg Lys Gly 245 250 255			768
ctg atc act gct cgg ttg cta gga gca aca gtc gca aca gct gaa acg Leu Ile Thr Ala Arg Leu Leu Gly Ala Thr Val Ala Thr Ala Glu Thr 260 265 270			816
ctc aca ttt tta gat gct cac tgt gag tgt ttc tat ggt tgg cta gaa Leu Thr Phe Leu Asp Ala His Cys Glu Cys Phe Tyr Gly Trp Leu Glu 275 280 285			864
cct ctg ttg gcc aga ata gct gag aac tac acg gct gtc gta agt cca Pro Leu Leu Ala Arg Ile Ala Glu Asn Tyr Thr Ala Val Val Ser Pro 290 295 300			912
gat att gca tcc ata gat ctg aac acg ttt gaa ttc aac aaa cct tct Asp Ile Ala Ser Ile Asp Leu Asn Thr Phe Glu Phe Asn Lys Pro Ser 305 310 315 320			960
cct tat gga agt aac cat aac cgt gga aat ttt gac tgg agt ctt tca Pro Tyr Gly Ser Asn His Asn Arg Gly Asn Phe Asp Trp Ser Leu Ser 325 330 335			1008
ttt ggc tgg gag tcg ctt cct gat cat gag aag caa aga agg aaa gat Phe Gly Trp Glu Ser Leu Pro Asp His Glu Lys Gln Arg Arg Lys Asp 340 345 350			1056
gaa acc tac cca att aaa aca ccc act ttt gca gga gga ctt ttt tcc Glu Thr Tyr Pro Ile Lys Thr Pro Thr Phe Ala Gly Gly Leu Phe Ser 355 360 365			1104
ata tca aaa gaa tat ttt gag tat att gga agc tat gat gaa gaa atg Ile Ser Lys Glu Tyr Phe Glu Tyr Ile Gly Ser Tyr Asp Glu Glu Met 370 375 380			1152
gaa atc tgg gga ggt gaa aat ata gaa atg tct ttc aga gta tgg caa Glu Ile Trp Gly Gly Glu Asn Ile Glu Met Ser Phe Arg Val Trp Gln 385 390 395 400			1200
tgt ggt ggg cag ttg gag att atg cct tgc tct gtt gtt gga cat gtt Cys Gly Gly Gln Leu Glu Ile Met Pro Cys Ser Val Val Gly His Val 405 410 415			1248
ttt cgc agc aaa agc cct cat agc ttt cca aaa ggc act cag gtg att Phe Arg Ser Lys Ser Pro His Ser Phe Pro Lys Gly Thr Gln Val Ile 420 425 430			1296
gct aga aac caa gtt cgc ctt gca gaa gtc tgg atg gat gaa tac aag Ala Arg Asn Gln Val Arg Leu Ala Glu Val Trp Met Asp Glu Tyr Lys			1344

435	440	445	
gaa ata ttt tat agg aga aat aca gat gca gca aaa att gtt aaa caa Glu Ile Phe Tyr Arg Arg Asn Thr Asp Ala Ala Lys Ile Val Lys Gln 450 455 460			1392
aaa gca ttt ggt gat ctt tca aaa aga ttt gaa ata aaa cac cgt ctt Lys Ala Phe Gly Asp Leu Ser Lys Arg Phe Glu Ile Lys His Arg Leu 465 470 475 480			1440
cgg tgt aaa aat ttt aca tgg tat ctg aac aac att tat cca gag gtg Arg Cys Lys Asn Phe Thr Trp Tyr Leu Asn Ile Tyr Pro Glu Val 485 490 495			1488
tat gtg cca gac ctt aat cct gtt ata tct gga tac att aaa agc gtt Tyr Val Pro Asp Leu Asn Pro Val Ile Ser Gly Tyr Ile Lys Ser Val 500 505 510			1536
ggt cag cct cta tgt ctg gat gtt gga gaa aac aat caa gga ggc aaa Gly Gln Pro Leu Cys Leu Asp Val Gly Glu Asn Asn Gln Gly Gly Lys 515 520 525			1584
cca tta att atg tat aca tgt cat gga ctt ggg gga aac cag tac ttt Pro Leu Ile Met Tyr Thr Cys His Gly Leu Gly Gly Asn Gln Tyr Phe 530 535 540			1632
gaa tac tct gct caa cat gaa att cgg cac aac atc cag aag gaa tta Glu Tyr Ser Ala Gln His Glu Ile Arg His Asn Ile Gln Lys Glu Leu 545 550 555 560			1680
tgt ctt cat gct gct caa ggt ctc gtt cag ctg aag gca tgt acc tac Cys Leu His Ala Ala Gln Gly Leu Val Gln Leu Lys Ala Cys Thr Tyr 565 570 575			1728
aaa ggt cac aag aca gtt gtc act gga gag cag ata tgg gag atc cag Lys Gly His Lys Thr Val Val Thr Gly Glu Gln Ile Trp Glu Ile Gln 580 585 590			1776
aag gat caa ctt cta tac aat cca ttc tta aaa atg tgc ctt tca gca Lys Asp Gln Leu Leu Tyr Asn Pro Phe Leu Lys Met Cys Leu Ser Ala 595 600 605			1824
aat gga gag cat cca agt tta gtg tca tgc aac cca tca gat cca ctc Asn Gly Glu His Pro Ser Leu Val Ser Cys Asn Pro Ser Asp Pro Leu 610 615 620			1872
caa aaa tgg ata ctt agc caa aat gat taa gtgttcctta aaattaagtt Gln Lys Trp Ile Leu Ser Gln Asn Asp 625 630			1922
gaaaaaggaa atattctttc tcataaaact gtgactaggc atacactgta gtttttgaaa			1982
attatgcaaaa agcagctaaa tgtaacttat tccaagtgca tttttcttat ttatatcttt			2042
atgtagcact actacagaaa ttctgcaagt ttctgtttca aagcacaata actagtaata			2102
ccaaagacta tttcaaaatg tccagatgta ggggaagaga tgtttacagt atgatgaaaa			2162
taattttcca agtaaagtga tgtttgtgtg ttttgtacac ttagggatat atatatatag			2222

ctacattcac	acactcacia	tttaaaatat	ttcccctagt	tttttggggg	gataggaaga	2282
aagatttggt	actgtatfff	tttaactaca	taaaaataga	tcaataaatg	tcagcattgg	2342
cctctgtgta	caaaccaaga	gctttttacag	atccagaatt	tattagtfta	aatgcaggt	2402
gaactttfff	ttgcgtttgg	tttacttgte	tgtcaaagt	ttccttaaac	atgaaactga	2462
ataaggagaa	gagtatfff	aacacttaaa	tttcttggea	aattttaaaa	catttttttag	2522
tctgtaatac	actccacttg	aagcacttaa	gtcttcctta	aatgactfff	cttaagtaat	2582
gatactgtgt	gttttcccaa	agcactftta	aaaaaatttt	tataaattac	tatctgttga	2642
aaagggtgtc	ttttcctftc	ttctagtatt	ttttttctta	ccaaaattca	ctaactttga	2702
atgtttgtga	tattaaattt	caaatgcaga	atacttgact	catttaaagc	taaattttgt	2762
tactgattca	attataattg	taatggattt	ttgactttgt	aatggattct	tttcatcaaa	2822
aagccttatt	attttttatc	tatgtggaaa	acacaataaa	aaatcctcaa	cactattgta	2882
atcatttggt	taagtgcfta	ttcctctftt	gggtaaaaatc	tgtaattgat	aatagggtggg	2942
ggaaaatgaa	ttttgtatgc	tgaatttcta	agcgcctatt	gtttgtaaaa	ccatcagata	3002
tttcttatgg	cacaaaaaat	gaggaatagc	aaaattcctg	tgttcaatat	ttagaaaatt	3062
ttgtattaat	ttctgataaa	gttccttaag	catctgatag	aatgatgttt	taaaaaaatt	3122
tgacgcttgc	ttaggagatt	taccactftt	tttttttggt	tttcgtcatt	ttatatftag	3182
atctcctgta	ttcttgfttc	cgaagtaaaa	tacgatcggg	ttcatatftt	aaatctggca	3242
gagcctcagc	tgtacgaaaa	agagcatata	ctgggttattg	accctatctt	ctcattgttt	3302
gtttgtaagt	ttgaatttgt	attaaaaagc	ctgcattctg	agctggacat	ggtggctcag	3362
cttctaattc	cagcactftg	gtaggcaaag	gtgggaggat	catttgagct	caggagttcc	3422
agaccagcct	gggcaacata	gcaaaatctc	atctctacaa	aaagtaaaaa	ttaaaaaatg	3482
aaattaaaaa	taaaattacc	taggtgtggg	ggcacgcata	tgtagttcca	gctatacagg	3542
aagggtgaggc	agaagcattg	cttgagcttg	ggagatcgag	gctacagtga	gctatgatta	3602
caccactgca	cttcagtctg	tgtgactgag	caagactctt	tcaaaaaaaaa	aaaaaagcct	3662
acattctcca	gttgattatt	tccaactaat	gtgtattatg	tgccctaattt	tctatcagaa	3722
gttgatttaa	gcccgtfttc	acactgctgt	taaagacata	cctgagactg	ggtaatttat	3782
aaagaaaaat	aggttcaatg	gacccacagg	tccgcgtggc	tggggaagct	tcacaatcat	3842
ggcggaagggt	gaaagcatgt	cttacgtgga	ag			3874

<210> 52
 <211> 633
 <212> PRT

<213> human

<400> 52

Met Ala His Leu Lys Arg Leu Val Lys Leu His Ile Lys Arg His Tyr
1 5 10 15

His Lys Lys Phe Trp Lys Leu Gly Ala Val Ile Phe Phe Phe Ile Ile
20 25 30

Val Leu Val Leu Met Gln Arg Glu Val Ser Val Gln Tyr Ser Lys Glu
35 40 45

Glu Ser Arg Met Glu Arg Asn Met Lys Asn Lys Asn Lys Met Leu Asp
50 55 60

Leu Met Leu Glu Ala Val Asn Asn Ile Lys Asp Ala Met Pro Lys Met
65 70 75 80

Gln Ile Gly Ala Pro Val Arg Gln Asn Ile Asp Ala Gly Glu Arg Pro
85 90 95

Cys Leu Gln Gly Tyr Tyr Thr Ala Ala Glu Leu Lys Pro Val Leu Asp
100 105 110

Arg Pro Pro Gln Asp Ser Asn Ala Pro Gly Ala Ser Gly Lys Ala Phe
115 120 125

Lys Thr Thr Asn Leu Ser Val Glu Glu Gln Lys Glu Lys Glu Arg Gly
130 135 140

Glu Ala Lys His Cys Phe Asn Ala Phe Ala Ser Asp Arg Ile Ser Leu
145 150 155 160

His Arg Asp Leu Gly Pro Asp Thr Arg Pro Pro Glu Cys Ile Glu Gln
165 170 175

Lys Phe Lys Arg Cys Pro Pro Leu Pro Thr Thr Ser Val Ile Ile Val
180 185 190

Phe His Asn Glu Ala Trp Ser Thr Leu Leu Arg Thr Val His Ser Val
195 200 205

Leu Tyr Ser Ser Pro Ala Ile Leu Leu Lys Glu Ile Ile Leu Val Asp
210 215 220

Asp	Ala	Ser	Val	Asp	Glu	Tyr	Leu	His	Asp	Lys	Leu	Asp	Glu	Tyr	Val
225					230					235					240
Lys	Gln	Phe	Ser	Ile	Val	Lys	Ile	Val	Arg	Gln	Arg	Glu	Arg	Lys	Gly
				245					250					255	
Leu	Ile	Thr	Ala	Arg	Leu	Leu	Gly	Ala	Thr	Val	Ala	Thr	Ala	Glu	Thr
			260					265					270		
Leu	Thr	Phe	Leu	Asp	Ala	His	Cys	Glu	Cys	Phe	Tyr	Gly	Trp	Leu	Glu
		275					280					285			
Pro	Leu	Leu	Ala	Arg	Ile	Ala	Glu	Asn	Tyr	Thr	Ala	Val	Val	Ser	Pro
	290					295					300				
Asp	Ile	Ala	Ser	Ile	Asp	Leu	Asn	Thr	Phe	Glu	Phe	Asn	Lys	Pro	Ser
305					310					315					320
Pro	Tyr	Gly	Ser	Asn	His	Asn	Arg	Gly	Asn	Phe	Asp	Trp	Ser	Leu	Ser
				325					330					335	
Phe	Gly	Trp	Glu	Ser	Leu	Pro	Asp	His	Glu	Lys	Gln	Arg	Arg	Lys	Asp
			340					345					350		
Glu	Thr	Tyr	Pro	Ile	Lys	Thr	Pro	Thr	Phe	Ala	Gly	Gly	Leu	Phe	Ser
		355					360					365			
Ile	Ser	Lys	Glu	Tyr	Phe	Glu	Tyr	Ile	Gly	Ser	Tyr	Asp	Glu	Glu	Met
	370					375					380				
Glu	Ile	Trp	Gly	Gly	Glu	Asn	Ile	Glu	Met	Ser	Phe	Arg	Val	Trp	Gln
385					390					395					400
Cys	Gly	Gly	Gln	Leu	Glu	Ile	Met	Pro	Cys	Ser	Val	Val	Gly	His	Val
				405					410					415	
Phe	Arg	Ser	Lys	Ser	Pro	His	Ser	Phe	Pro	Lys	Gly	Thr	Gln	Val	Ile
			420					425					430		
Ala	Arg	Asn	Gln	Val	Arg	Leu	Ala	Glu	Val	Trp	Met	Asp	Glu	Tyr	Lys
		435					440					445			
Glu	Ile	Phe	Tyr	Arg	Arg	Asn	Thr	Asp	Ala	Ala	Lys	Ile	Val	Lys	Gln
	450					455					460				

Lys Ala Phe Gly Asp Leu Ser Lys Arg Phe Glu Ile Lys His Arg Leu
 465 470 475 480

Arg Cys Lys Asn Phe Thr Trp Tyr Leu Asn Asn Ile Tyr Pro Glu Val
 485 490 495

Tyr Val Pro Asp Leu Asn Pro Val Ile Ser Gly Tyr Ile Lys Ser Val
 500 505 510

Gly Gln Pro Leu Cys Leu Asp Val Gly Glu Asn Asn Gln Gly Gly Lys
 515 520 525

Pro Leu Ile Met Tyr Thr Cys His Gly Leu Gly Gly Asn Gln Tyr Phe
 530 535 540

Glu Tyr Ser Ala Gln His Glu Ile Arg His Asn Ile Gln Lys Glu Leu
 545 550 555 560

Cys Leu His Ala Ala Gln Gly Leu Val Gln Leu Lys Ala Cys Thr Tyr
 565 570 575

Lys Gly His Lys Thr Val Val Thr Gly Glu Gln Ile Trp Glu Ile Gln
 580 585 590

Lys Asp Gln Leu Leu Tyr Asn Pro Phe Leu Lys Met Cys Leu Ser Ala
 595 600 605

Asn Gly Glu His Pro Ser Leu Val Ser Cys Asn Pro Ser Asp Pro Leu
 610 615 620

Gln Lys Trp Ile Leu Ser Gln Asn Asp
 625 630

<210> 53
 <211> 20
 <212> DNA
 <213> Artificial Sequence Sequence

<220>
 <223> chemically-synthesized oligonucleotide primer

<400> 53
 ccgcacgaca accgcaccat

20

<210> 54
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> chemically-synthesized oligonucleotide primer

 <400> 54
 cgctccggcc cacaaatctc 20

<210> 55
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> chemically-synthesized oligonucleotide primer

 <400> 55
 ctccaatcgt ccctacagtc g 21

<210> 56
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> chemically-synthesized oligonucleotide primer

 <400> 56
 ccaagctatc acctcggcc 19

<210> 57
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> chemically-synthesized oligonucleotide primer

 <400> 57
 tgtttctgca atggtgaggt g 21

<210> 58
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> chemically-synthesized oligonucleotide primer

 <400> 58
 gcggctccaa gacttcctaa t 21

<210> 59
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> chemically-synthesized oligonucleotide primer

 <400> 59
 gctgccctaa agccaaactc t 21

 <210> 60
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> chemically-synthesized oligonucleotide primer

 <400> 60
 agaggacagg gaggatcaag ttc 23

 <210> 61
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> chemically-synthesized oligonucleotide primer

 <400> 61
 tggcgacact taccgagctt 20

 <210> 62
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> chemically-synthesized oligonucleotide primer

 <400> 62
 ccatgcccct tgtagtagct gta 23

 <210> 63
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> chemically-synthesized oligonucleotide primer

 <400> 63
 cttgactgtg gttactgctg atca 24

 <210> 64
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> chemically-synthesized oligonucleotide primer

 <400> 64
 gtatccaccg aatgtgaaaa cgt 23

<210> 65
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> chemically-synthesized oligonucleotide primer

 <400> 65
 tgtccctcgg aaaaactggt 20

<210> 66
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> chemically-synthesized oligonucleotide primer

 <400> 66
 agccaccgtt catggtctct 20

<210> 67
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> chemically-synthesized oligonucleotide primer

 <400> 67
 agaacggcac gcctacgat 19

<210> 68
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> chemically-synthesized oligonucleotide primer

 <400> 68
 aggtagcctt tgctgtactc atcat 25

<210> 69
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> chemically-synthesized oligonucleotide primer

 <400> 69
 tcacctgatt cttgcgtgct 20

<210> 70
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> chemically-synthesized oligonucleotide primer

 <400> 70
 ctgtgggtta ttatcaatct tgtttctt 28

<210> 71
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> chemically-synthesized oligonucleotide primer

 <400> 71
 gcatgtacaa tggctgcg 19

<210> 72
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> chemically-synthesized oligonucleotide primer

 <400> 72
 caagagctgt aaacggcgg 19

<210> 73
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> chemically-synthesized oligonucleotide primer

 <400> 73
 gagacaccat tgagacttga ccag 24

<210> 74
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> chemically-synthesized oligonucleotide primer

 <400> 74
 caccaagatg aaggttcggg 20

 <210> 75
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> chemically-synthesized oligonucleotide primer

 <400> 75
 tgtgacagcc agctcgaaaa c 21

 <210> 76
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> chemically-synthesized oligonucleotide primer

 <400> 76
 tggagagcca agacttttcc a 21

 <210> 77
 <211> 19
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> chemically-synthesized oligonucleotide primer

 <400> 77
 gcctgccatt ctcagcaaa 19

 <210> 78
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> chemically-synthesized oligonucleotide primer

 <400> 78
 aactgaatc caccaggac a 21

 <210> 79
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> chemically-synthesized oligonucleotide primer

 <400> 79
 caagtccttc cggcatgaa 19

<210> 80
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> chemically-synthesized oligonucleotide primer

 <400> 80
 ccaaaatcac ccttcctttg c 21

<210> 81
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> chemically-synthesized oligonucleotide primer

 <400> 81
 cttgacaaca cagcagcgtc a 21

<210> 82
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> chemically-synthesized oligonucleotide primer

 <400> 82
 acttgaagat gtggaggccc a 21

<210> 83
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> chemically-synthesized oligonucleotide primer

 <400> 83
 tgggtcaagaa agcaccaatg c 21

<210> 84
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> chemically-synthesized oligonucleotide primer

 <400> 84
 ccacacacgc catcttttctt c 21

<210> 85
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> chemically-synthesized oligonucleotide primer

 <400> 85
 ttgtctataa caccgcgcct g 21

<210> 86
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> chemically-synthesized oligonucleotide primer

 <400> 86
 cggcgtggaa aataggagag t 21

<210> 87
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> chemically-synthesized oligonucleotide primer

 <400> 87
 aggagaagaa gctggcagga g 21

<210> 88
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> chemically-synthesized oligonucleotide primer

 <400> 88
 cttgatggcg ttggtgagc 19

<210> 89
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> chemically-synthesized oligonucleotide primer

 <400> 89
 tgggtaccgt atgcctcga 19

 <210> 90
 <211> 19
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> chemically-synthesized oligonucleotide primer

 <400> 90
 tgtattcaaa ggtgggccg 19

 <210> 91
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> chemically-synthesized oligonucleotide primer

 <400> 91
 tgctgggaca tgtaccgtca t 21

 <210> 92
 <211> 19
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> chemically-synthesized oligonucleotide primer

 <400> 92
 ccagatgcgg tagccatca 19

 <210> 93
 <211> 19
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> chemically-synthesized oligonucleotide primer

 <400> 93
 gccttctctg tgcacggag 19

 <210> 94
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> chemically-synthesized oligonucleotide primer

 <400> 94
 gtgagaccag cccaaagaca c 21

<210> 95
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> chemically-synthesized oligonucleotide primer

 <400> 95
 atgggagttg gtagggaccg 20

<210> 96
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> chemically-synthesized oligonucleotide primer

 <400> 96
 catgggaggg tgatccactt 20

<210> 97
 <211> 19
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> chemically-synthesized oligonucleotide primer

 <400> 97
 ggctgcattg aaggcatgt 19

<210> 98
 <211> 19
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> chemically-synthesized oligonucleotide primer

 <400> 98
 aagggcaaac tccacaggc 19

<210> 99
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> chemically-synthesized oligonucleotide primer

 <400> 99
 ttacccggaa gcgtatgtgc 20

 <210> 100
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> chemically-synthesized oligonucleotide primer

 <400> 100
 gcctccctgg ttattctcac c 21

 <210> 101
 <211> 32
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> chemically-synthesized oligonucleotide primer

 <400> 101
 gcggccgcac catgaggggc aaccactga tc 32

 <210> 102
 <211> 29
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> chemically-synthesized oligonucleotide primer

 <400> 102
 gcggccgcct agaaggcact gttccatga 29

 <210> 103
 <211> 36
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> chemically-synthesized oligonucleotide primer

 <400> 103
 gacgcgttgc ggccgcagca tggcggatac cggctt 36

 <210> 104
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> chemically-synthesized oligonucleotide primer

 <400> 104
 aaaggatggc ggccgctcac tcgctgtcga atttga 36

<210> 105
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> chemically-synthesized oligonucleotide primer

 <400> 105
 gcggccgcag catggaccgc gcggggcgc 29

<210> 106
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> chemically-synthesized oligonucleotide primer

 <400> 106
 atgcatctag acagaaggcc ttggaggag 29

<210> 107
 <211> 32
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> chemically-synthesized oligonucleotide primer

 <400> 107
 gcggccgcag gatgggatgc gtgaagtcca gg 32

<210> 108
 <211> 44
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> chemically-synthesized oligonucleotide primer

 <400> 108
 gcggccgctc aaggctgctg ctggaactgg ctctcagtgg ccgt 44

<210> 109
 <211> 32
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> chemically-synthesized oligonucleotide primer

 <400> 109
 gcggccgcag aatggctcac cttaggac ta 32

 <210> 110
 <211> 32
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> chemically-synthesized oligonucleotide primer

 <400> 110
 gcggccgctt attcattttg gctaaaaatc ca 32

 <210> 111
 <211> 33
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> chemically-synthesized oligonucleotide primer

 <400> 111
 cggagcatgg cggataccgg cttgcgccgc gtg 33

 <210> 112
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> chemically-synthesized oligonucleotide primer

 <400> 112
 gcgcaagccg gtatccgcca t 21

 <210> 113
 <211> 21
 <212> RNA
 <213> Artificial Sequence

 <220>
 <223> chemically-synthesized oligonucleotide primer

 <400> 113
 auggcggauc ccggcuugcg c 21

 <210> 114
 <211> 21
 <212> RNA
 <213> Artificial Sequence

<220>

<223> chemically-synthesized oligonucleotide primer

<400> 114

gcgcaagccg guaucgcga u

21